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| HBJCJ82 | 9509 | 779645 | AL161456 | 42415 | 1-1118 |
| HBJCJ82 | 9509 | 779645 | AL158075 | 42416 | 1-1523 |
| HBJCJ82 | 9509 | 779645 | AL158075 | 42417 | 1-853 1340-2553 |
| HBJCJ82 | 9509 | 779645 | AL158075 | 42418 | 1-482 |
| HBJCE07 | 9510 | 954090 | AC025605 | 42419 | 1-357 443-919 |
| HBJCE07 | 9510 | 954090 | AC073101 | 42420 | 1-357 |
| HBJCE07 | 9510 | 954090 | AC025605 | 42421 | 1-653 |
| HBJCE07 | 9510 | 954090 | AC073101 | 42422 | 1-233 |
| HBJCE07 | 9510 | 954090 | AC073101 | 42423 | 1-420 |
| HBJBR04 | 9512 | 847952 | AC005682 | 42424 | 1-458 |
| HBJBR04 | 9512 | 847952 | AC005682 | 42425 | 1-373 |
| HBJAP95 | 9513 | 796659 | AL138715 | 42426 | 1-1044 |
| HBJAP95 | 9513 | 796659 | AL031601 | 42427 | 1-590 1338-1600 |

| | | | | | |
|---------|------|--------|----------|-------|-----------|
| | | | | | 2644-3247 |
| HBJAP95 | 9513 | 796659 | AL138715 | 42428 | 1-717 |
| HBJAP95 | 9513 | 796659 | AL138715 | 42429 | 1-265 |
| HBJAP95 | 9513 | 796659 | AL031601 | 42430 | 1-706 |
| HBJAJ49 | 9515 | 723164 | AC078846 | 42431 | 1-416 |
| | | | | | 1103-1882 |
| HBJAJ49 | 9515 | 723164 | AC078846 | 42432 | 1-116 |
| HBJAH27 | 9517 | 682941 | AC016325 | 42433 | 1-69 |
| | | | | | 560-632 |
| | | | | | 2298-2395 |
| | | | | | 2510-2613 |
| | | | | | 3563-3801 |
| | | | | | 5031-5598 |
| | | | | | 5763-5801 |
| HBJAE32 | 9518 | 699695 | AC044843 | 42434 | 1-487 |
| | | | | | 983-1447 |
| HBJAE32 | 9518 | 699695 | AC008525 | 42435 | 1-487 |
| | | | | | 983-1447 |
| HBJAE32 | 9518 | 699695 | AC008525 | 42436 | 1-337 |
| HBJAB49 | 9520 | 722195 | AF276759 | 42437 | 1-1613 |
| HBJAB49 | 9520 | 722195 | AC019031 | 42438 | 1-1613 |
| HBJAB49 | 9520 | 722195 | AF276759 | 42439 | 1-561 |
| HBJAB49 | 9520 | 722195 | AC019031 | 42440 | 1-561 |
| HBJAB28 | 9521 | 847966 | AC023071 | 42441 | 1-736 |
| HBJAB15 | 9522 | 660552 | AP001931 | 42442 | 1-1266 |
| HBJAB15 | 9522 | 660552 | AP000727 | 42443 | 1-1264 |
| HBJAB15 | 9522 | 660552 | AP001931 | 42444 | 1-366 |
| HBJAB15 | 9522 | 660552 | AP001931 | 42445 | 1-308 |
| HBJAB15 | 9522 | 660552 | AP000727 | 42446 | 1-366 |
| HBJAB15 | 9522 | 660552 | AP000727 | 42447 | 1-308 |
| HBD4E47 | 9523 | 720008 | AL353776 | 42448 | 1-1591 |
| HBD4E47 | 9523 | 720008 | AL353776 | 42449 | 1-490 |
| HBDAD16 | 9525 | 661560 | AC013396 | 42450 | 1-1371 |
| HBDAD16 | 9525 | 661560 | AC013396 | 42451 | 1-296 |
| HBDAD16 | 9525 | 661560 | AC013396 | 42452 | 1-204 |
| HBCCO10 | 9526 | 963157 | AC009634 | 42453 | 1-575 |
| HBCCO10 | 9526 | 963157 | AC011721 | 42454 | 1-575 |
| HBCCO10 | 9526 | 963157 | AC009634 | 42455 | 1-206 |
| HBCCO10 | 9526 | 963157 | AC011721 | 42456 | 1-206 |
| HBCCO10 | 9526 | 963157 | AC011721 | 42457 | 1-86 |
| HBCCJ05 | 9527 | 930956 | AC068322 | 42458 | 1-600 |
| HBCCJ05 | 9527 | 930956 | AC027243 | 42459 | 1-600 |
| HBCCJ05 | 9527 | 930956 | AC024059 | 42460 | 1-600 |
| HBCCJ05 | 9527 | 930956 | AC010868 | 42461 | 1-584 |
| HBCCJ05 | 9527 | 930956 | AC068322 | 42462 | 1-424 |
| HBCCJ05 | 9527 | 930956 | AC027243 | 42463 | 1-456 |
| HBCCJ05 | 9527 | 930956 | AC068322 | 42464 | 1-460 |
| | | | | | 1112-1585 |
| HBCCJ05 | 9527 | 930956 | AC027243 | 42465 | 1-460 |
| | | | | | 1112-1585 |
| HBCCJ05 | 9527 | 930956 | AC024059 | 42466 | 1-456 |
| HBCCJ05 | 9527 | 930956 | AC010868 | 42467 | 1-385 |
| HBCCJ05 | 9527 | 930956 | AC010868 | 42468 | 1-335 |
| HBCCD06 | 9529 | 938319 | AC007783 | 42469 | 1-2334 |
| | | | | | 2508-3084 |
| | | | | | 3578-3890 |

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|---------|------|--------|----------|-------|--|
| | | | | | 4198-4294 4376-4623 4712-5349 5369-6088 6527-7107 7298-7392 7730-7846 9147-9476 10487-10575 10791-11298 11485-11601 11783-13009 13207-13501 13540-13772 14439-14800 14923-14983 15133-15355 15485-15653 16750-16805 16894-17078 17162-17219 18003-18089 21085-21146 21358-21501 |
| HBCCD06 | 9529 | 938319 | AC007783 | 42470 | 1-308 |
| HBCCD06 | 9529 | 938319 | AC007783 | 42471 | 1-1024 |
| HBCCB51 | 9530 | 975256 | AL139353 | 42472 | 1-71 265-794 1791-2077 2409-2656 |
| HBCBN51 | 9532 | 952057 | AC073846 | 42473 | 1-141 323-951 1073-1625 1640-2371 |
| HBCBN51 | 9532 | 952057 | AC073846 | 42474 | 1-285 |
| HBCBF12 | 9535 | 969578 | AC068735 | 42475 | 1-530 |
| HBCBF12 | 9535 | 969578 | AC021725 | 42476 | 1-534 |
| HBCBF12 | 9535 | 969578 | AL021368 | 42477 | 1-382 762-1102 1231-1761 |
| HBCBF12 | 9535 | 969578 | AC068735 | 42478 | 1-342 |
| HBCBF12 | 9535 | 969578 | AC021725 | 42479 | 1-342 |
| HBCBF12 | 9535 | 969578 | AC068735 | 42480 | 1-659 |
| HBCBF12 | 9535 | 969578 | AC021725 | 42481 | 1-679 |
| HBCBF12 | 9535 | 969578 | AL021368 | 42482 | 1-664 |
| HBCBF12 | 9535 | 969578 | AL021368 | 42483 | 1-307 |
| HBCBE57 | 9536 | 848322 | AL031666 | 42484 | 1-1235 |
| HBCBE57 | 9536 | 848322 | AL031666 | 42485 | 1-508 |
| HBCBE57 | 9536 | 848322 | AL031666 | 42486 | 1-648 |
| HBCBB22 | 9537 | 848325 | AC010735 | 42487 | 1-900 |
| HBCAT10 | 9539 | 968195 | AL357521 | 42488 | 1-374 |
| HBCAT10 | 9539 | 968195 | AL021528 | 42489 | 1-374 |
| HBCAT10 | 9539 | 968195 | AL357521 | 42490 | 1-689 |
| HBCAT10 | 9539 | 968195 | AL357521 | 42491 | 1-355 |
| HBCAT10 | 9539 | 968195 | AL021528 | 42492 | 1-689 |
| HBCAT10 | 9539 | 968195 | AL021528 | 42493 | 1-355 |

| | | | | | |
|---------|------|--------|----------|-------|--|
| HBCAS32 | 9540 | 699489 | AC007101 | 42494 | 1-215 867-1214 1226-2260 2359-2415 |
| HBCAQ85 | 9541 | 783431 | AC019071 | 42495 | 1-831 1116-1365 1600-1920 2161-2334 2902-3156 3364-3836 4074-4278 4306-4417 4485-4581 4693-4853 4995-5264 5758-5863 6411-6509 6551-6922 |
| HBCAQ85 | 9541 | 783431 | AC019071 | 42496 | 1-412 |
| HASCG58 | 9543 | 738423 | AC011116 | 42497 | 1-869 |
| HASCG58 | 9543 | 738423 | AC078794 | 42498 | 1-870 |
| HASCG58 | 9543 | 738423 | AC011116 | 42499 | 1-971 |
| HASCG58 | 9543 | 738423 | AC078794 | 42500 | 1-623 |
| HASCG58 | 9543 | 738423 | AC011116 | 42501 | 1-623 |
| HASAW90 | 9544 | 789112 | AC010234 | 42502 | 1-2931 |
| HASAW90 | 9544 | 789112 | AC021464 | 42503 | 1-58 332-547 909-1209 2280-2634 3445-3539 4477-4620 7577-10496 12087-13447 13462-15091 15142-16137 |
| HASAW90 | 9544 | 789112 | AC021464 | 42504 | 1-506 |
| HASAC10 | 9546 | 968746 | AC007677 | 42505 | 1-477 |
| HASAC10 | 9546 | 968746 | AC007677 | 42506 | 1-1410 |

[052] Table 1B summarizes additional polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:) contig nucleotide sequence identifiers (SEQ ID NO:X)), and genomic sequences (SEQ ID NO:B). The first column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA clone related to each contig sequence. The second column provides the sequence identifier, "SEQ ID NO:X", for each contig sequence. The third column provides a unique contig identifier, "Contig ID:" for each contig sequence. The fourth column, provides a BAC identifier "BAC ID NO:A" for the BAC clone referenced in the corresponding row of the table. The fifth column provides the nucleotide sequence identifier, "SEQ ID NO:B" for a fragment of the BAC clone identified in column four of the corresponding row of the table. The sixth column, "Exon From-To", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:B which delineate certain polynucleotides of the invention that are also exemplary members of polynucleotide sequences that encode polypeptides of the invention (e.g., polypeptides containing amino acid sequences encoded by the polynucleotide sequences delineated in column six, and fragments and variants thereof).

TABLE 2

| Clone ID NO:Z | Contig ID: | SEQ ID NO:X | Analysis Method | PFam/NR Description | PFam/NR Accession Number | Score/ Percent Identity | NT From | NT To |
|------------------|---------------|-------------------|-----------------------------|--|--|---------------------------------------|---------------------------------|------------------------------------|
| HAMHB21 | 961376 | 11 | HMMER 2.1.1 | PFAM: RhoGAP domain | PF00620 | 100 | 497 | 916 |
| HBDAC79 | 935414 | 26 | HMMER 2.1.1 blastx.14 | PFAM: Acyl-CoA dehydrogenase (AL021958) fadE9 [Mycobacterium tuberculosis] | PF00441 gi 2911026 emb CAA 17519.1 | 102.6 62% 51% 64% 35% | 94 94 250 348 6 | 342 255 384 422 89 |
| HBJAG72 | 722723 | 32 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 2.32 | 83 | 115 |
| HBJGT92 | 919507 | 107 | HMMER 1.8 | PFAM: Bacterial mut protein | PF00293 | 7.68 | 377 | 436 |
| HBJIY20 | 669519 | 141 | HMMER 2.1.1 | PFAM: Orn/Lys/Arg decarboxylase | PF01276 | 53.1 | 49 | 162 |
| HBMBU24 | 677240 | 234 | HMMER 1.8 | PFAM: Core histones H2A, H2B, H3 and H4 | PF00125 | 7.72 | 139 | 192 |
| HBMZ71 | 880580 | 238 | HMMER 1.8 | PFAM: von Willebrand factor type D domain | PF00094 | 26.52 | 200 | 526 |
| HBMDC16 | 888206 | 258 | blastx.2 | Butyrophilin-like protein BUTR-1. | sp AAF72554 AAF72 554 | 50% | 19 | 315 |
| HBMUO90 | 928078 | 294 | blastx.14 | Zfp61p [Mus musculus] | gi 887887 gb AAC52 290.1 | 84% 53% | 24 154 | 119 243 |
| HBMXE31 | 573323 | 317 | HMMER 1.8 | PFAM: Gonadotropin- releasing hormones | PF00446 | 10.78 | 112 | 141 |
| HCFCF47 | 894415 | 372 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF00069 | 89.54 | 20 | 295 |
| HCFCJ21 | 671028 | 374 | HMMER | PFAM: Core histones | PF00125 | 12.79 | 123 | 188 |

| | | | | | | | | |
|---------|--------|-----|-----------------------------|---|--------------------------------------|---|---|---|
| HCFLE95 | 945122 | 391 | 1.8 blastx.14 | H2A, H2B, H3 and H4 p34 protein [Rattus sp.] | gi 534876 dbj BAA02786.1 | 81% 100% 85% | 126 236 71 | 191 271 91 |
| HCUAL07 | 953876 | 449 | blastx.14 | (AF079098) arginine-tRNA-protein transferase 1-1p; ATE1-1p [Homo sapiens] | gi 3806094 gb AAD12366.1 | 87% | 5 | 97 |
| HCUBJ11 | 967484 | 478 | blastx.14 | Ps 2=basic proline-rich protein(PRB1L precursor 1 1 [Homo sapiens] | gi 386433 gb AAB27289.1 | 37% 53% 35% 40% 28% 40% 36% 36% 41% 41% 32% 33% 36% 36% 71% 71% 35% | 158 62 325 133 158 133 225 225 74 74 325 158 158 183 44 44 74 | 63 24 242 59 63 59 160 160 24 24 242 87 93 118 24 24 24 |
| HCUDT65 | 915742 | 548 | HMMER 2.1.1 blastx.14 | PFAM: tRNA synthetases class II (A) ORF YNL040w [Saccharomyces cerevisiae] | PF01411 gi 1301892 emb CAA95907.1 | 35.1 42% 52% 31% 42% | 697 763 658 1153 1678 | 930 972 759 1293 1740 |

| | | | | | | | | | | |
|---------|--------|-----|----------------|--|--|-------------------------------|--|--------------------|--------------------|--------------------|
| HCUEU10 | 964857 | 595 | HMMER 1.8 | | PFAM: Bacterial regulatory proteins, luxR family | PF00196 | | 21% 20% 5.43 | 1009 1273 13 | 1149 1494 42 |
| HCUGB48 | 880730 | 647 | HMMER 1.8 | | PFAM: TNFR/NGFR cysteine-rich region | PF00020 | | 7.99 | 173 | 226 |
| HCUGR38 | 706471 | 670 | HMMER 1.8 | | PFAM: Alcohol/other dehydrogenases, short chain type | PF00106 | | 73.02 | 102 | 284 |
| HCUHM44 | 615198 | 702 | HMMER 1.8 | | PFAM: HMG (high mobility group) box | PF00505 | | 4.81 | 2 | 73 |
| HCWAK80 | 702435 | 748 | HMMER 1.8 | | PFAM: Src homology domain 3 | PF00018 | | 3.55 | 316 | 387 |
| HCWAR05 | 932623 | 759 | blastx.14 | | hypothetical protein [Synechocystis sp.] | gi 1653272 dbj BAA1 8187.1 | | 47% 46% 71% | 235 70 321 | 83 32 301 |
| HCWBB63 | 667283 | 782 | HMMER 2.1.1 | | PFAM: Secretory protein of YscJ/FliF family | PF01514 | | 78.2 | 45 | 275 |
| HCWBE76 | 968515 | 799 | HMMER 1.8 | | PFAM: Helix-loop-helix DNA-binding domain | PF00010 | | 9.77 | 13 | 51 |
| HCWBI37 | 967717 | 809 | blastx.14 | | URF (pot. 4.5S protein) [Escherichia coli] | gi 42759 emb CAA25 537.1 | | 63% 85% 60% | 9 202 228 | 179 222 257 |
| HCWBI53 | 934909 | 810 | blastx.14 | | lepA [Mycobacterium tuberculosis] | gi 1655655 emb CAB 03723.1 | | 85% 84% | 65 9 | 166 65 |
| HCWBI90 | 921653 | 812 | blastx.14 | | xylose isomerase [Klebsiella pneumoniae] | gi 43952 emb CAA43 389.1 | | 59% 55% | 316 344 | 8 291 |
| HCWBN06 | 924638 | 825 | blastx.14 | | collagen type XVII [Mus musculus] | gi 309183 gb AAA37 443.1 | | 26% 46% | 153 262 | 266 306 |

| | | | | | | | | | |
|---------|--------|------|----------------|---|-------------------------------|--|-------|-----|-----|
| HCWBQ03 | 920886 | 834 | blastx.14 | ORF YBR208c [Saccharomyces cerevisiae] | | | 57% | 5 | 46 |
| | | | | | | | 36% | 75 | 140 |
| | | | | | | | 46% | 259 | 303 |
| | | | | | | | 43% | 310 | 357 |
| | | | | | | | 75% | 337 | 360 |
| | | | | | | | 42% | 78 | 119 |
| HCWCM65 | 529230 | 891 | HMMER 1.8 | PFAM: AMP-binding enzymes | gi 536588 emb CAA8 5172.1 | | 69.62 | 31 | 264 |
| HCWCR31 | 693632 | 909 | HMMER 2.1.1 | PFAM: ATP synthase (E/31 kDa) subunit | PF01991 | | 80 | 229 | 381 |
| HCWDI64 | 924632 | 945 | blastx.14 | tetracycline transporter- like protein [Mus musculus] | gi 2506078 dbj BAA2 2622.1 | | 82% | 117 | 167 |
| | | | | | | | 87% | 73 | 120 |
| HCWDJ23 | 527555 | 952 | HMMER 2.1.1 | PFAM: Bacterial extracellular solute- binding proteins, family 3 | PF00497 | | 27.3 | 25 | 198 |
| HCWDL45 | 889416 | 957 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | | 4.63 | 121 | 168 |
| HCWDR01 | 839104 | 973 | HMMER 1.8 | PFAM: ABC transporters | PF00005 | | 62.98 | 15 | 179 |
| | | | blastx.2 | (AE000411) putative ATP-binding component of a transport system [Escherichia coli] | gb AAC76377.1 | | 69% | 9 | 215 |
| | | | | | | | 44% | 18 | 200 |
| | | | | | | | 51% | 281 | 373 |
| | | | | | | | 41% | 391 | 477 |
| HCWDV17 | 974478 | 993 | HMMER 1.8 | PFAM: Bacterial regulatory proteins, luxR family | PF00196 | | 81.59 | 416 | 613 |
| HCWDX22 | 967361 | 1014 | blastx.14 | copC peptide | gi 151190 gb AAA25 | | 79% | 365 | 84 |

| | | | | | | | | |
|---------|--------|------|---------------------------|--|---|----------------------|-----------------|------------------|
| HCWDX76 | 932614 | 1019 | blastx.14 | [Pseudomonas syringae] (AF102543) unknown [Zymomonas mobilis] | 808.1 gi 4378174 gb AAD1 9419.1 | 81% | 423 | 358 |
| HCWED61 | 971865 | 1041 | blastx.14 | gp210 (AA 1-1886) [Rattus norvegicus] | gi 56463 emb CAA68 759.1 | 75% | 481 | 212 |
| HCWEG69 | 948693 | 1058 | HMMER 1.8 blastx.14 | PFAM: Zinc-binding metalloprotease domain orf3 [Pseudomonas aeruginosa] | PF00099 gi 557259 emb CAA5 7572.1 | 2.79 55% 87% | 57 248 56 | 98 45 9 |
| HCWEI19 | 948690 | 1066 | HMMER 1.8 blastx.14 | PFAM: Zinc-binding metalloprotease domain formaldehyde dehydrogenase (glutathione) [Escherichia coli] | PF00099 gi 887431 emb CAA5 2057.1 | 8.6 75% | 226 300 | 273 10 |
| HCWEL01 | 916972 | 1086 | blastx.14 | (AF010496) exonuclease SbcD homolog [Rhodobacter capsulatus] | gi 3128267 gb AAC1 6119.1 | 39% 47% | 34 193 | 171 249 |
| HCWEM51 | 920887 | 1096 | blastx.14 | argininosuccinate lyase [Bacillus subtilis] | gi 2635409 emb CAB 14904.1 | 54% 47% | 365 57 | 39 7 |
| HCWEQ14 | 908245 | 1105 | HMMER 1.8 blastx.14 | PFAM: DEAD and DEAH box helicases (AC002985) R27090_2 [Homo sapiens] | PF00270 gi 2443870 gb AAB8 1544.1 | 72.08 100% 66% | 37 37 5 | 177 177 40 |
| HCWEW45 | 571355 | 1116 | HMMER 1.8 blastx.14 | PFAM: Heat shock hsp90 proteins | PF00183 | 10.32 | 37 | 186 |
| HCWEY34 | 954142 | 1125 | blastx.14 | (AJ000758) precorrin-4 methylase [Bacillus megaterium] | gi 3724045 emb CAA 04314.1 | 32% | 3 | 242 |

| | | | | | | | | |
|---------|--------|------|---------------------------|---|--------------------------------------|-------------------|------------------|-------------------|
| HCWFF88 | 506577 | 1143 | HMMER 1.8 | PFAM: Src homology domain 3 | PF00018 | 4.92 | 140 | 181 |
| HCWFK57 | 861907 | 1149 | HMMER 2.1.1 | PFAM: RNA polymerase beta subunit | PF00562 | 36.2 | 34 | 270 |
| HCWFT29 | 690751 | 1186 | HMMER 1.8 | PFAM: Helicases conserved C-terminal domain | PF00271 | 4.51 | 105 | 152 |
| HCWFU66 | 853005 | 1196 | HMMER 2.1.1 | PFAM: Aldehyde dehydrogenase family | PF00171 | 71.4 | 105 | 269 |
| HCWGB78 | 861843 | 1217 | HMMER 2.1.1 | PFAM: Ribosomal protein L31 | PF01197 | 50.8 | 126 | 236 |
| HCWGE12 | 967067 | 1223 | HMMER 1.8 | PFAM: Bacterial mufT protein | PF00293 | 4.04 | 214 | 288 |
| HCWGW12 | 964088 | 1262 | blastx.14 | L-lactate dehydrogenase (EC 1.1.1.27) - Acinetobacter 1 | pir A37334 A37334 | 73% | 137 | 60 |
| HCWGY90 | 960159 | 1288 | HMMER 1.8 blastx.14 | PFAM: Bacterial regulatory helix-loop- helix proteins, araC family operon regulatory protein [Erwinia carotovora] | PF00165 gi 48382 gb AA24 811.1 | 58.7 86% | 6 6 | 137 158 |
| HCWHB12 | 970688 | 1295 | blastx.14 | Nodulation protein V (EC 2.7.3.-). [Escherichia coli] | gi 1736771 dbj BAA1 5920.1 | 47% 33% 85% | 195 59 310 | 314 211 330 |
| HCWHD07 | 953384 | 1305 | blastx.14 | Isp42p [Saccharomyces cerevisiae] | gi 736300 emb CAA8 8644.1 | 41% 46% 50% | 56 298 341 | 301 393 394 |
| HCWHP74 | 598510 | 1334 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 2.09 | 68 | 112 |

| | | | | | | | | |
|---------|--------|------|----------------|--|---------------------------|------|---|---|
| HCWHQ03 | 924187 | 1336 | blastx.14 | (AL049608) extensin-like protein [Arabidopsis thaliana] | gi 4584539 emb CAB40769.1 | 50% | 85 | 14 206 126 253 247 218 |
| HCWHQ31 | 574945 | 1337 | HMMER 2.1.1 | PFAM: Carbon-nitrogen hydrolase | PF00795 | 39.4 | 141 | 308 |
| HCWHR81 | 935419 | 1343 | HMMER 2.1.1 | PFAM: Ribosomal protein L30p/L7e | PF00327 | 90.5 | 107 | 265 |
| HCWHT59 | 924105 | 1349 | blastx.14 | (AF047828) syringomycin synthetase [Pseudomonas syringae pv. syringae] | gi 3510629 gb AAC80285.1 | 57% | 261 327 261 261 122 122 329 157 104 104 107 142 305 249 249 305 157 157 311 107 246 | 148 148 148 148 9 9 252 104 9 9 252 104 9 9 107 252 160 160 252 107 107 249 15 163 |
| HCWK08 | 959388 | 1388 | blastx.14 | pot. ORF 1 [Homo] | gi 1335196 emb CAA | 57% | 83 | 27 |

| | | | | | | | | |
|---------|--------|------|-----------|--|---------------------------|-------|-----|-----|
| | | | | sapiens] | 26917.1] | 62% | 303 | 256 |
| HCWKN08 | 959380 | 1409 | blastx.14 | CeoB [Burkholderia cepacia] | gi 2109271 gb AAB58161.1 | 55% | 249 | 169 |
| | | | | | | 50% | 148 | 83 |
| | | | | | | 62% | 281 | 258 |
| | | | | | | 54% | 61 | 29 |
| HCWKV68 | 959801 | 1427 | blastx.14 | (AL121600) hypothetical protein SCF76.09 1 | gi 6002364 emb CAB56729.1 | 34% | 219 | 142 |
| | | | | | | 42% | 120 | 43 |
| | | | | | | 57% | 238 | 218 |
| HCWLD06 | 935392 | 1437 | blastx.14 | ORF_o485 [Escherichia coli] | gi 887832 gb AAA83063.1 | 47% | 240 | 7 |
| | | | | | | 42% | 449 | 282 |
| | | | | | | 35% | 66 | 7 |
| HCWLE37 | 960093 | 1442 | blastx.14 | (AF039571) peripheral benzodiazepine receptor interacting protein; PBR-IP/PRAX1 [Homo sapiens] | gi 4104812 gb AAD11957.1 | 100% | 126 | 263 |
| | | | | | | 85% | 304 | 345 |
| | | | | | | 87% | 103 | 126 |
| | | | | | | 44% | 66 | 119 |
| | | | | | | 36% | 250 | 315 |
| HCWLH79 | 959458 | 1453 | blastx.14 | (AC004877) sco-spondin-mucin-like; similar to p98167 1 sapiens] | gi 3638957 gb AAC36301.1 | 27% | 289 | 191 |
| | | | | | | 71% | 326 | 306 |
| HCWTB11 | 965024 | 1462 | blastx.14 | DNA primase [Escherichia coli] | gi 147755 gb AAA24600.1 | 45% | 341 | 3 |
| HCWTB56 | 853009 | 1470 | HMMER 1.8 | PFAM: E1-E2 ATPases | PF00122 | 55.15 | 2 | 301 |
| | | | blastx.2 | cadmium resistance protein [Lactococcus lactis] | gb AAB37345.1 | 42% | 2 | 316 |
| HCWTR08 | 958791 | 1516 | blastx.14 | (AE000888) malate dehydrogenase [Methanobacterium | gi 2622314 gb AAB85694.1 | 43% | 66 | 134 |
| | | | | | | 44% | 182 | 262 |

| | | | | | | | | |
|---------|--------|------|----------------|---|---|----------------------------|------------------------|--------------------------|
| HCWTR54 | 729290 | 1517 | HMMER 1.8 | thermoautotrophicum] PFAM: Helicases conserved C-terminal domain | PF00271 | 6.14 | 151 | 198 |
| HCWTS15 | 654317 | 1519 | HMMER 1.8 | PFAM: D-isomer specific 2-hydroxyacid dehydrogenases | PF00389 | 47.52 | 2 | 166 |
| HCWUU16 | 661570 | 1593 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 2.17 | 33 | 77 |
| HDDMA83 | 926991 | 1633 | blastx.14 | (AF038963) RNA helicase [Homo sapiens] | gi 4405795 gb AAD1 9826.1 | 100% 51% 100% 90% | 2 537 656 526 | 514 635 694 558 |
| HDMAQ15 | 941282 | 1646 | HMMER 2.1.1 | PFAM: POT family | PF00854 | 77.2 | 811 | 386 |
| HDPAG32 | 947832 | 1655 | blastx.2 | (AF121080) cAMP inducible 1 protein [Mus musculus] | gb AAD24570.1 AF1 21080_1 | 80% | 2 | 997 |
| HDPCN94 | 794275 | 1678 | HMMER 2.1.1 | PFAM: Peptidase family M1 | PF01433 | 39.1 | 335 | 577 |
| HDPFF07 | 974494 | 1694 | blastx.14 | PFAM: RhoGEF domain | PF00621 | 54.2 | 363 | 740 |
| HDPIT53 | 926498 | 1736 | blastx.14 | (AF151363) Cdc42 GTPase-activating protein [Mus musculus] | gi 5020264 gb AAD3 8043.1 AF151363_1 | 92% 96% 50% | 513 715 458 | 716 789 505 |
| HDPIT61 | 741724 | 1737 | blastx.2 | (AF109719) BAT2 [Mus musculus] | gi 3941737 gb AAC8 2480.1 | 50% 30% | 229 278 | 170 219 |
| | | | | (AF121080) cAMP inducible 1 protein [Mus musculus] | gb AAD24570.1 AF1 21080_1 | 73% 57% | 48 293 | 329 397 |

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|---------|--------|------|----------------|--|-------------------------------|-------------------|-----------------|------------------|
| HDPKD52 | 959653 | 1750 | HMMER 1.8 | PFAM: Fibronectin type III domain | PF00041 | 4.82 | 340 | 402 |
| HDPLC45 | 909091 | 1755 | HMMER 2.1.1 | PFAM: BTB/POZ domain | PF00651 | 39.5 | 280 | 507 |
| HDPMA48 | 582015 | 1775 | blastx.2 | (AF038007) FIC1 [Homo sapiens] | gb AAC63461.1 | 54% | 152 | 703 |
| HDPMO62 | 912722 | 1780 | HMMER 1.8 | PFAM: Ras family (contains ATP/GTP binding P-loop) | PF00071 | 132.39 | 127 | 432 |
| | | | blastx.2 | rab-related GTP-binding protein [Homo sapiens] | emb CAA68227.1 | 54% 57% | 133 20 | 444 76 |
| HDPNC96 | 934520 | 1788 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF00069 | 206.63 | 3 | 734 |
| | | | blastx.14 | HUMAN NDR [unidentified] | gi 2304746 emb CAA 03387.1 | 92% | 3 | 734 |
| HDPOJ93 | 792193 | 1797 | HMMER 1.8 | PFAM: EF hand | PF00036 | 7.78 | 266 | 313 |
| HDPPP24 | 812091 | 1815 | HMMER 2.1.1 | PFAM: Fes/CIP4 homology domain | PF00611 | 22.4 | 151 | 387 |
| HDPPU44 | 951276 | 1818 | HMMER 1.8 | PFAM: Lectin C-type domain short and long forms | PF00059 | 37.49 | 245 | 376 |
| HDPRH02 | 919404 | 1837 | blastx.14 | ORF YGR090w [Saccharomyces cerevisiae] | gi 1323133 emb CAA 97093.1 | 30% 48% | 266 593 | 451 673 |
| | | | blastx.14 | reverse transcriptase [Homo sapiens] | gi 439877 gb AAB02 291.1 | 66% 37% 54% | 6 280 235 | 59 351 267 |
| HDPTW90 | 722699 | 1868 | HMMER 1.8 | PFAM: IG (immunoglobulin) | PF00047 | 3.32 | 1 | 24 |

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|---------|--------|------|----------------------------|--|-------------------------------|--|--|--|
| HDPVG11 | 966556 | 1877 | HMMER 1.8 | superfamily PFAM: PH (pleckstrin homology) domain | PF00169 | 16 | 518 | 613 |
| HDPWE80 | 909916 | 1890 | HMMER 2.1.1 blastx.2 | PFAM: PH domain (AF102854) membrane- associated guanylate kinase-interacting protein 2 Maguin-2 [Rattus norvegicus] | PF00169 gb AAD04568.1 | 81.2 36% | 412 | 708 |
| HDPWY46 | 915964 | 1894 | blastx.14 | (AF061738) leucine aminopeptidase [Homo sapiens] | gi 4335941 gb AAD1 7527.1 | 94% 87% 80% 95% 62% 33% | 3 316 140 254 425 305 | 152 438 217 316 472 358 |
| HDQEF04 | 927024 | 1914 | blastx.14 | Bassoon [Mus musculus] | gi 3413810 emb CAA 76598.1 | 75% | 239 | 216 |
| HDQGT70 | 909848 | 1936 | blastx.14 | Bat2 [Homo sapiens] | gi 29375 emb CAA78 744.1 | 37% | 248 | 201 |
| HDQHT10 | 963481 | 1944 | blastx.14 | (AF039571) peripheral benzodiazepine receptor interacting protein; PBR- IP/PRAX1 [Homo sapiens] | gi 4104812 gb AAD1 1957.1 | 58% 43% 100% 55% 42% 58% 83% | 490 387 76 253 256 45 51 | 455 319 59 227 215 10 34 |
| HDQHZ10 | 961336 | 1945 | blastx.14 | fractionated X-irradiation- induced 29 thymoma [Mus musculus] | gi 1389694 gb AAB0 2905.1 | 51% 71% | 47 2 | 256 43 |
| HDQHZ22 | 879416 | 1946 | blastx.2 | cysteine rich hair keratin | emb CAA56339.1 | 40% | 65 | 319 |

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|---------|--------|------|----------------|---|------------------------------|--|---------------------------|-------------------------|--------------------------|
| | | | | | | | 42% | 65 | 352 |
| HDTAY23 | 973925 | 1956 | blastx.14 | associated protein [Oryctolagus cuniculus] (AF086624) serine threonine kinase [Rattus norvegicus] | gi 3800869 gb AAC6 8900.1 | | 98% | 78 | 254 |
| HDTAY23 | 974565 | 9561 | blastx.14 | (AF086624) serine threonine kinase [Rattus norvegicus] | gi 3800869 gb AAC6 8900.1 | | 98% 85% 100% 66% | 79 330 371 305 | 255 371 403 331 |
| HDTBO48 | 945083 | 1959 | HMMER 1.8 | PFAM: IG (immunoglobulin) superfamily | PF00047 | | 18.53 | 159 | 347 |
| | | | blastx | (AJ009698) embigin protein [Rattus norvegicus] | emb CAA08796.1 | | 58% 75% 58% | 132 273 357 | 248 356 464 |
| HDTBR50 | 846630 | 1968 | HMMER 1.8 | PFAM: Thioredoxins | PF00085 | | 29.85 | 163 | 297 |
| HDTBY88 | 934472 | 1973 | HMMER 2.1.1 | PFAM: Eukaryotic protein kinase domain | PF00069 | | 93.6 | 3 | 302 |
| | | | blastx.14 | p56 KIAMRE protein kinase [Homo sapiens] | gi 1517820 gb AAC5 0918.1 | | 82% 35% 100% | 3 192 492 | 170 458 509 |
| HDTDC53 | 916348 | 1977 | HMMER 1.8 | PFAM: Core histones H2A, H2B, H3 and H4 | PF00125 | | 7.98 | 180 | 233 |
| HDTEI19 | 912765 | 1984 | blastx.14 | rab4b [Canis familiaris] | gi 919 emb CAA3980 0.1 | | 78% 88% | 244 387 | 354 413 |
| HDTES50 | 964709 | 1987 | HMMER 1.8 | PFAM: RNA recognition motif. (aka RRM, RBD, or RNP domain) | PF00076 | | 31.58 | 108 | 326 |
| | | | blastx.2 | arginine-rich nuclear | gb AAA35554.1 | | 65% | 36 | 350 |

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|---------|--------|------|--------------|---|-------------------------------|---|--|---|
| HDTHQ15 | 923899 | 2009 | blastx.14 | protein [Homo sapiens] Similar to a C.elegans protein encoded in cosmid C27F2 (U40419) [Homo sapiens] | gi 1665781 dbj BAA1 3387.1 | 97% | 4 | 612 |
| HDTHZ46 | 957669 | 2012 | blastx.14 | (AC004877) sco-spondin- mucin-like; similar to p98167 1 sapiens] | gi 3638957 gb AAC3 6301.1 | 43% 42% 46% 43% 40% 38% | 100 45 172 2 5 318 | 168 101 216 49 49 371 |
| HDTID61 | 908946 | 2016 | HMMER 1.8 | PFAM: Zinc finger, C2H2 type | PF000096 | 7.07 | 407 | 430 |
| | | | blastx.2 | (AK002053) unnamed protein product [Homo sapiens] | dbj BAA92059.1 | 46% 53% 50% 45% 47% 49% 46% 33% 42% 34% 51% 57% 37% 32% 50% 47% 66% | 45 45 33 45 45 48 45 18 18 60 18 347 347 338 374 338 519 | 389 341 341 389 344 356 344 674 320 554 245 457 547 553 457 442 554 |
| HDTIF01 | 883070 | 2017 | blastx.2 | (AF010144) neuronal | gb AAC08737.1 | 61% | 315 | 524 |

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|---------|--------|------|--------------|--|---|--|--|--|-------|-----|-----|
| | | | | | thread protein AD7c-NTP [Homo sapiens] | | | | 61% | 309 | 509 |
| | | | | | | | | | 65% | 361 | 507 |
| | | | | | | | | | 62% | 34 | 162 |
| | | | | | | | | | 60% | 53 | 172 |
| | | | | | | | | | 41% | 304 | 507 |
| | | | | | | | | | 35% | 286 | 507 |
| | | | | | | | | | 40% | 327 | 473 |
| | | | | | | | | | 50% | 50 | 151 |
| | | | | | | | | | 57% | 89 | 166 |
| | | | | | | | | | 47% | 109 | 171 |
| | | | | | | | | | 37% | 308 | 379 |
| | | | | | | | | | 52% | 128 | 178 |
| HDTIZ44 | 925574 | 2032 | blastx.14 | procollagen alpha 2(V) [Homo sapiens] | gi 2370202 emb CAA 75002.1 | | | | 43% | 77 | 9 |
| | | | | | | | | | 40% | 89 | 9 |
| | | | | | | | | | 37% | 89 | 9 |
| | | | | | | | | | 57% | 229 | 188 |
| | | | | | | | | | 47% | 183 | 133 |
| | | | | | | | | | 60% | 135 | 106 |
| | | | | | | | | | 47% | 328 | 278 |
| | | | | | | | | | 75% | 165 | 142 |
| | | | | | | | | | 60% | 121 | 92 |
| | | | | | | | | | 43% | 139 | 92 |
| | | | | | | | | | 54% | 165 | 133 |
| | | | | | | | | | 60% | 162 | 133 |
| | | | | | | | | | 54% | 226 | 194 |
| HDTJ137 | 799834 | 2036 | HMMER 1.8 | PFAM: Laminin B (Domain IV) | PF00052 | | | | 2.02 | 386 | 466 |
| HDTJJ02 | 913787 | 2037 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | | | | 5.7 | 21 | 68 |
| HDTKQ14 | 886936 | 2044 | HMMER | PFAM: Src homology | PF00018 | | | | 12.87 | 430 | 546 |

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|---------|--------|------|-------------|--|----------------------------|--|--|---|
| HDTLD17 | 908601 | 2052 | 1.8 | domain 3 | emb CAB41255.1 PF00096 | 100% 56% 96.3 | 439 76 154 | 555 291 222 |
| | | | blastx.2 | (AL049683) hypothetical protein [Homo sapiens] | | | | |
| | | | HMMER 2.1.1 | PFAM: Zinc finger, C2H2 type | | | | |
| | | | blastx.2 | Zfp-29 [Mus musculus] | emb CAA38920.1 | 48% 65% 66% 66% 65% 62% 64% 47% 58% 42% 50% 47% 47% 48% 43% 42% 46% 35% 43% 43% 46% 63% 63% 52% 56% 35% | 49 49 49 70 49 49 70 115 49 372 375 375 375 372 372 372 375 279 372 375 375 547 547 538 547 375 | 636 399 399 399 411 369 381 636 324 641 569 569 569 569 578 602 569 569 569 569 636 636 651 642 491 |
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|---------|--------|------|-------------|---|---------------------------|---------------------------------|--------------------------------|------------------------------|
| HEOMG48 | 963338 | 2091 | blastx.14 | very large tegument protein [human herpesvirus 2] | gi 1869859 emb CAB06722.1 | 66% | 641 | 667 |
| HEOMG78 | 920911 | 2092 | blastx.14 | contains similarity to C2 domains [Caenorhabditis elegans] | gi 1825586 gb AAB42222.1 | 70% 40% | 294 136 | 437 246 |
| HEOMS08 | 959581 | 2113 | blastx.14 | (AF034970) docking protein [Homo sapiens] | gi 3043919 gb AAC13265.1 | 93% 83% | 129 172 | 173 207 |
| HEOMT79 | 936687 | 2118 | blastx.14 | (AF108420) 1-aminocyclopropane-carboxylate synthase [Fugu rubripes] | gi 4426837 gb AAD20564.1 | 52% | 10 | 210 |
| HEOMU79 | 965900 | 2121 | blastx.14 | HLA-B-associated transcript 2 (BAT2) [Homo sapiens] | gi 179339 gb AAA35585.1 | 29% | 320 | 198 |
| HEOMX92 | 919200 | 2131 | blastx.14 | TGR-CL5bis [Homo sapiens] | gi 1247469 emb CAA01862.1 | 53% 38% 53% 30% 27% | 274 129 271 44 206 | 230 91 233 6 174 |
| HEOMX92 | 961148 | 9562 | blastx.14 | retrovirus-related reverse transcriptase pseudogene - slow loris | pir B25313 GNLRL1 | 46% 50% | 44 247 | 241 312 |
| HEONQ19 | 930705 | 2142 | HMMER 2.1.1 | PFAM: PH domain | PF00169 | 42.5 | 213 | 533 |
| | | | blastx.2 | (AJ250425) Collybistin I [Rattus norvegicus] | emb CAB65966.1 | 96% | 9 | 629 |

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|---------|--------|------|-------------------------|---|---------------------------|--|--|--|
| HEONV59 | 949152 | 2148 | blastx.2 | (AK001463) unnamed protein product [Homo sapiens] | dbj BAA91707.1 | 51% 50% | 163 284 | 279 379 |
| HEOPE58 | 851009 | 2157 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 5.32 | 320 | 364 |
| HEOPO08 | 958184 | 2174 | blastx.14 | alpha-1 type II collagen [Xenopus laevis] | gi 214044 gb AAA49679.1 | 38% 32% 31% 75% 36% | 142 429 429 273 208 | 11 346 334 250 134 |
| HEOQC76 | 909032 | 2189 | HMMER 2.1.1 blastx.2 | PFAM: Zinc finger, C2H2 type (AK001753) unnamed protein product [Homo sapiens] | PF00096 dbj BAA91884.1 | 86.9 37% 33% 35% 52% 29% | 169 139 139 139 154 196 | 237 609 609 480 306 582 |
| HEOQP44 | 942596 | 2203 | HMMER 2.1.1 | PFAM: Beta-lactamase | PF00144 | 420.7 | 250 | 1026 |
| HEOQS11 | 965930 | 2204 | blastx.14 | ORF1A [Homo sapiens] | gi 475909 emb CAA47472.1 | 51% | 30 | 152 |
| HEORE79 | 959572 | 2214 | blastx.14 | rehydrin [Tortula ruralis] | gi 1732471 gb AAB49656.1 | 53% 46% 50% 50% 55% 55% 42% 62% 62% 62% | 101 101 232 284 58 180 223 58 180 302 | 145 145 267 325 84 206 264 81 203 325 |

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|---------|--------|------|----------------|--|-------------------------------------|-------------|--------------|--------------|
| HHECO01 | 915285 | 2250 | blastx.14 | (AF039691) antigen NY-CO-9 [Homo sapiens] | gi 3170182 gb AAC18040.1 | 65% 100% | 302 25 | 174 2 |
| HHEEC07 | 952455 | 2267 | blastx.14 | (AF064257) Dhml-like protein [Homo sapiens] | gi 5881961 gb AAD55138.1 AF064257.1 | 99% 100% | 1202 1862 | 1801 1912 |
| HHEHU73 | 923895 | 2279 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 4.1 | 115 | 156 |
| HHEJH30 | 961974 | 2282 | blastx.14 | (AF180920) cyclin ania-6a [Homo sapiens] | gi 5823554 gb AAD53184.1 AF180920.1 | 95% 95% | 226 429 | 417 494 |
| HHEHD45 | 919630 | 2302 | HMMER 1.8 | PFAM: Double-stranded RNA binding motif | PF00035 | 12.86 | 25 | 114 |
| | | | blastx.14 | [D.melanogaster mRNA, complete cds.], gene product [Drosophila melanogaster] | gi 158506 gb AAA73062.1 | 52% 47% | 1 235 | 114 297 |
| HHEQK01 | 871911 | 2346 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 3.27 | 64 | 90 |
| HHEQV39 | 932851 | 2354 | HMMER 1.8 | PFAM: Src homology domain 3 | PF00018 | 30.41 | 526 | 708 |
| HHESU85 | 783820 | 2381 | HMMER 1.8 | PFAM: Heat shock hsp90 proteins | PF00183 | 11.81 | 88 | 288 |
| HHETQ54 | 908567 | 2392 | HMMER 2.1.1 | PFAM: KRAB box | PF01352 | 166.4 | 233 | 421 |
| | | | blastx.14 | NK10 [Mus musculus] | gi 506502 emb CAA56225.1 | 89% | 212 | 448 |
| HHEUA62 | 965709 | 2400 | HMMER 1.8 | PFAM: Spectrin alpha chain, repeated domain | PF00435 | 10.48 | 103 | 186 |
| | | | blastx.14 | (AB023622) Septin6 [Mus musculus] | gi 5689158 dbj BAA82838.1 | 59% 60% | 13 211 | 144 315 |

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|---------|--------|------|----------------|--|---|--|--|---------------------------------------|
| HHEUC31 | 795268 | 2401 | HMMER 2.1.1 | PFAM: Ank repeat | PF00023 | 31.5 | 3 | 92 |
| HKBAT27 | 963724 | 2486 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 2.17 | 11 | 37 |
| HLMBW11 | 950728 | 2526 | blastx.14 | (AF156884) RIP-like kinase [Homo sapiens] | gi 5059425 gb AAD3 9005.1 AF156884_1 | 92% | 129 | 782 |
| HLMBY16 | 531053 | 2529 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 1.99 | 82 | 123 |
| HLMDU71 | 531228 | 2572 | HMMER 2.1.1 | PFAM: Phosphate- binding protein | PF01449 | 48.1 | 1 | 123 |
| HLMFU09 | 909666 | 2600 | blastx.14 | (AF151363) Cdc42 GTPase-activating protein [Mus musculus] | gi 5020264 gb AAD3 8043.1 AF151363_1 | 78% | 277 | 372 |
| HLMHP67 | 967636 | 2633 | blastx.14 | Hypothetical bacteriophage n4 receptor protein NfrA precursor. [Escherichia coli] | gi 1651236 dbj BAA3 5202.1 | 82% 100% | 107 3 | 340 104 |
| HLMHT94 | 531054 | 2641 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 2.86 | 264 | 284 |
| HLMIX95 | 960056 | 2679 | blastx.14 | (AB008430) CDEP [Homo sapiens] | gi 2766165 dbj BAA2 4267.1 | 89% 69% | 440 47 | 330 9 |
| HLMMA52 | 920292 | 2694 | blastx.14 | ORF-3 protein [Pseudorabies virus] | gi 334072 gb AAA47 471.1 | 43% 100% 70% | 115 165 174 | 162 176 203 |
| HLMMD05 | 932127 | 2697 | blastx.14 | collagen [Ascaris suum] | gi 159657 gb AAA29 371.1 | 50% 61% 44% 58% 63% 50% | 189 355 189 107 349 387 | 124 317 115 72 317 352 |

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|----------|--------|------|----------------|---|------------------------------|--|--|---|
| HLMMV66 | 926188 | 2733 | HMMER 1.8 | PFAM: Ank repeat | PF00023 | 42% 50% 46% 46% 32% 46% | 358 407 355 110 189 355 | 317 366 317 66 115 317 |
| | | | blastx.14 | similar to HUMORFU (D26069) [Homo sapiens] | gi 488505 dbj BAA06 418.1 | 62% 81% 86% 71% 39% 43% | 230 337 404 378 173 99 | 382 384 448 419 256 146 |
| HLMNL55 | 964739 | 2769 | blastx.14 | dynein heavy chain isotype 6 [Tripneustes gratilla] | gi 687206 gb AAA63 589.1 | 70% 37% | 19 184 | 138 231 |
| HLMNN02 | 920296 | 2776 | blastx.14 | (AF083501) latent nuclear antigen [Macaca mulatta rhadinovirus 17577] | gi 4494984 gb AAD2 1406.1 | 36% 53% 50% 33% | 345 191 86 306 | 289 153 57 208 |
| HL YAA41 | 909874 | 2871 | HMMER 2.1.1 | PFAM: PH domain | PF00169 | 37.3 | 162 | 260 |
| HL YDL60 | 909866 | 2980 | blastx.14 | ORF-3 protein [Pseudorabies virus] | gi 334072 gb AAA47 471.1 | 44% 37% 35% 30% 39% 75% 47% 75% | 89 229 376 259 283 179 232 26 | 15 158 293 191 215 156 182 3 |

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|----------|--------|------|-------------|---|---------------------------|-------|-----|-----|
| HL YDS11 | 966732 | 2986 | blastx.14 | orfIV [Borna disease virus] | gi 473842 gb AAA20666.1 | 38% | 250 | 197 |
| HL YDT68 | 526245 | 2991 | HMMER 1.8 | PFAM: Zinc finger, C2H2 type | PF00096 | 38% | 223 | 161 |
| HL YDV62 | 927872 | 2993 | HMMER 2.1.1 | PFAM: PH domain | PF00169 | 39% | 200 | 3 |
| | | | blastx.2 | (AC005496) unknown protein [Arabidopsis thaliana] | gb AAC35236.1 | 4.11 | 89 | 124 |
| HL YEN93 | 682176 | 3005 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 58.6 | 188 | 406 |
| HL YGP46 | 832311 | 3042 | HMMER 2.1.1 | PFAM: IQ calmodulin-binding motif | PF00612 | 41% | 113 | 292 |
| HL YHN67 | 920551 | 3056 | blastx.14 | EDTP(egg derived tyrosine phosphatase). | sp BAA33720 BAA33720 | 38% | 451 | 504 |
| HMAAF10 | 968199 | 3062 | blastx.14 | Formate c-acetyltransferase (EC 2.3.1.54). [Escherichia coli] | gi 1651427 dbj BAA35638.1 | 2.86 | 383 | 409 |
| | | | | | | 100% | 1 | 300 |
| | | | | | | 76% | 347 | 385 |
| HMABJ56 | 907640 | 3063 | HMMER 2.1.1 | PFAM: ADP-ribosylation factor family | PF00025 | 24.4 | 157 | 231 |
| | | | blastx.14 | (AF082517) ADP-ribosylation factor [Entamoeba histolytica] | gi 3746799 gb AAC64063.1 | 39% | 281 | 403 |
| HMABQ71 | 729831 | 3065 | HMMER 2.1.1 | PFAM: DNA topoisomerase II (N-terminal region) | PF00204 | 56% | 154 | 228 |
| | | | | | | 61% | 233 | 271 |
| | | | | | | 128.8 | 210 | 407 |

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|----------|--------|------|-------------|--|---------------------------|-------|------|------|
| HMADC02 | 920088 | 3067 | blastx.14 | ORF_f418 [Escherichia coli] | gi 536985 gb AAA97040.1 | 95% | 202 | 143 |
| HMADZ55 | 939916 | 3071 | blastx.2 | (AK002022) unnamed protein product [Homo sapiens] | dbj BAA92041.1 | 98% | 270 | 728 |
| HMAFY42 | 778521 | 3078 | HMMER 2.1.1 | PFAM: WH1 domain | PF00568 | 90 | 46 | 303 |
| HMAGK69 | 723186 | 3080 | HMMER 1.8 | PFAM: Signal C terminal domain | PF00512 | 40.87 | 31 | 405 |
| HMAIC22 | 947905 | 3085 | HMMER 2.1.1 | PFAM: Peptidase family M3 | PF01432 | 65.9 | 115 | 402 |
| HMAKA11 | 966282 | 9569 | blastx.14 | CG Site No. 18031 [Escherichia coli] | gi 466635 gb AAB18474.1 | 84% | 112 | 390 |
| | | | | | | 100% | 2 | 112 |
| | | | | | | 55% | 363 | 422 |
| HMAKA11 | 966282 | 9569 | blastx.14 | MaoB [Escherichia coli] | gi 1480003 dbj BAA11058.1 | 99% | 1516 | 803 |
| | | | | | | 90% | 1673 | 1545 |
| HMALL66 | 956195 | 3091 | HMMER 1.8 | PFAM: Adenylate kinases | PF00406 | 50.17 | 1587 | 1474 |
| HMCDN22 | 895981 | 3107 | blastx.2 | (AJ007798) stromal antigen 3, (STAG3) [Homo sapiens] | emb CAB59367.1 | 82% | 85 | 456 |
| | | | | | | 90% | 445 | 573 |
| HMCFB22 | 963794 | 3110 | blastx.14 | probable transposase - human transposon MER37 | pir S72481 S72481 | 71% | 10 | 168 |
| | | | | | | 73% | 183 | 320 |
| | | | | | | 82% | 119 | 187 |
| HMCYG77 | 753133 | 3117 | HMMER 2.1.1 | PFAM: Kelch motif | PF01344 | 43% | 313 | 423 |
| | | | | | | 61% | 5 | 58 |
| HMMAAB49 | 462502 | 3127 | HMMER | PFAM: Zinc-binding | PF00099 | 63% | 90 | 122 |
| | | | | | | 51.9 | 7 | 132 |
| | | | | | | 3.49 | 166 | 183 |

| | | | | | | | | | |
|----------|--------|------|-----------|---|---|--------------------------|-------------------|-------------------|-------------------|
| HMMAC19 | 953580 | 3129 | 1.8 | blastx.14 | metallopeptidase domain (AF003535) ORF2-like protein [Homo sapiens] | gi 2197085 gb AAD04635.1 | 47% | 26 | 145 |
| HMMCH04 | 944069 | 3208 | blastx.2 | unknown [Homo sapiens] | gb AAC50940.1 | | 58% | 423 | 680 |
| HMQBU96 | 765162 | 3247 | HMMER 1.8 | PFAM: Helix-loop-helix DNA-binding domain | PF00010 | | 7.33 | 8 | 40 |
| HMQDZ19 | 940694 | 3267 | blastx.14 | urokinase plasminogen activator receptor [Homo sapiens] | gi 433901 emb CAA52191.1 | | 100% 91% | 89 133 | 124 168 |
| HMSBV28 | 970579 | 3303 | blastx.14 | YKL249 [Saccharomyces cerevisiae] | gi 871536 emb CAA49304.1 | | 92% 51% 50% | 260 141 323 | 108 1 282 |
| HMSCD15 | 918133 | 3310 | HMMER 1.8 | PFAM: Src homology domain 3 | PF00018 | | 41.06 | 453 | 599 |
| HMSFR69 | 738588 | 3373 | HMMER 1.8 | PFAM: Core histones H2A, H2B, H3 and H4 | dbj BAA91451.1 | | 98% 29% 28% | 453 387 80 | 635 479 175 |
| HMSGGL27 | 855759 | 9573 | HMMER 1.8 | PFAM: Bacterial mutT protein | PF00293 | | 5.56 | 276 | 202 |
| HMSGP73 | 925385 | 3401 | blastx.14 | (AC004490) R29381_1 [Homo sapiens] | gi 2995577 gb AAC08316.1 | | 94% 95% | 141 901 | 908 972 |
| HMSGX14 | 871492 | 3413 | HMMER 1.8 | PFAM: Ribosomal protein S12 | PF00164 | | 33.44 | 28 | 153 |
| HMSHO64 | 746582 | 3431 | HMMER 1.8 | PFAM: Src homology domain 3 | PF00018 | | 11.08 | 316 | 405 |
| | | | blastx.2 | (AF030131) Plenty of SH3s; POSH [Mus] | gb AAC40070.1 | | 47% | 1 | 411 |

| | | | | | | | | |
|---------|--------|------|----------------|--|---|---------------------------------|---------------------------------|----------------------------------|
| HMSHZ56 | 733386 | 3447 | HMMER 1.8 | musculus] PFAM: Zinc finger, CCHC class | PF00098 | 4.89 | 208 | 228 |
| HMSJT11 | 965007 | 3491 | blastx.14 | (AF148805) latent nuclear antigen [Kaposi sarcoma- associated herpesvirus] | gi 5669894 gb AAD4 6501.1 AF148805_6 | 20% 24% 21% 23% 16% | 667 241 241 211 139 | 1137 465 465 453 465 |
| HMSJW19 | 744990 | 3498 | HMMER 2.1.1 | PFAM: BAH domain | PF01426 | 48.7 | 2 | 163 |
| HMSKI08 | 959413 | 3509 | blastx.14 | (AF094516) E1-like protein [Homo sapiens] | gi 3820614 gb AAC6 9630.1 | 97% | 97 | 513 |
| HMSOM08 | 958216 | 3538 | blastx.14 | (AF082556) TRF1 - interacting ankyrin-related ADP-ribose polymerase [Homo sapiens] | gi 3929219 gb AAC7 9841.1 | 76% | 2 | 232 |
| HMSOU92 | 948130 | 9578 | blastx.2 | (AF118082) PRO1902 [Homo sapiens] | gb AAF22026.1 AF1 18094_21 | 64% 63% 88% | 302 462 532 | 463 527 558 |
| HMSOX47 | 948202 | 3548 | blastx.14 | cDNA EST EMBL:M89462 comes from this gene; cDNA EST 1 1 yk349d7.5 comes from this gene; cDNA EST yk358b9.5 comes from this | gi 3879085 emb CAA 94301.1 | 48% 39% 36% 39% 26% | 514 365 266 173 514 | 612 463 355 256 591 |
| HMVDU16 | 904807 | 3589 | HMMER 1.8 | PFAM: Core histones H2A, H2B, H3 and H4 | PF00125 | 13.38 | 1252 | 1329 |
| HMWCQ09 | 924634 | 3606 | blastx.14 | Emf1 alpha [Ephydatia muelleri] | gi 9300 emb CAA494 72.1 | 50% 33% 66% | 19 99 217 | 84 233 243 |

| | | | | | | | | |
|---------|--------|------|-----------|---|-------------------------------------|---------------------------------|------------------------------|--------------------------------|
| HMWDD54 | 932261 | 3610 | blastx.14 | (AF175223) SANT domain protein SMRTER [Drosophila melanogaster] | gi 5815245 gb AAD52614.1 AF175223_1 | 38% | 292 | 345 |
| HMWDF88 | 906769 | 3612 | HMMER 1.8 | PFAM: Low-density lipoprotein receptor domain class A | PF00057 | 41.61 | 171 | 245 |
| | | | blastx.14 | (AF110520) NG29 [Mus musculus] | gi 4050096 gb AAC97969.1 | 69% 48% 35% 50% | 114 129 9 72 | 239 239 110 107 |
| HMWGG55 | 920575 | 3642 | blastx.14 | DNA polymerase [Pyrococcus furiosus] | gi 216918 dbj BAA02362.1 | 94% | 195 | 308 |
| HMWGT07 | 953454 | 3645 | blastx.14 | (AL078579) putative protein [Arabidopsis thaliana] | gi 4972120 emb CAB43977.1 | 40% 40% 46% | 218 395 113 | 322 475 157 |
| HMWHN70 | 851334 | 3654 | HMMER 1.8 | PFAM: Zinc finger, C3HC4 type (RING finger) | PF00097 | 6.51 | 187 | 255 |
| HNEBJ08 | 958742 | 3689 | blastx.14 | mucin 2 precursor, intestinal - human (fragments) | pir A49963 A43932 | 35% 83% | 305 320 | 264 303 |
| HNEDU01 | 909832 | 3748 | blastx.14 | (AC002398) F25965_3 [Homo sapiens] | gi 2477513 gb AAB81198.1 | 71% 57% 62% 43% 50% | 207 80 1 323 337 | 323 205 87 412 384 |
| HNFEF95 | 971171 | 3792 | blastx.14 | ORF_o493 [Escherichia coli] | gi 606260 gb AAA58123.1 | 98% 89% 81% | 548 103 185 | 201 20 105 |
| HNFFM25 | 705856 | 3818 | HMMER | PFAM: Laminin B | PF00052 | 0.47 | 520 | 603 |

| | | | | | | | | |
|---------|--------|------|-----------------------------|---|---|---|--|---|
| HNFFT62 | 574623 | 3828 | 1.8 HMMER 1.8 | (Domain IV) PFAM: C2 domain | PF00168 | 2.74 | 207 | 272 |
| HNFGI01 | 921431 | 3851 | blastx.14 | (AF118890) s-tomosyn isoform [Rattus norvegicus] | gi 4689231 gb AAD2 7819.1 AF118890_1 | 86% 100% 40% | 234 153 287 | 302 200 361 |
| HNFGI49 | 909707 | 3852 | blastx.14 | (AF086624) serine threonine kinase [Rattus norvegicus] | gi 3800869 gb AAC6 8900.1 | 100% 100% | 1 60 | 45 86 |
| HNFGM76 | 908665 | 3862 | HMMER 2.1.1 blastx.2 | PFAM: Zinc finger, C2H2 type (AF132599) RANTES factor of late activated T lymphocytes-1 [Homo sapiens] | PF00096 gb AAD26864.1 AF1 32599_1 | 74.8 92% | 232 1 | 306 417 |
| HNFHA11 | 967520 | 3874 | HMMER 2.1.1 blastx.14 | PFAM: Phosphoenolpyruvate carboxykinase phosphoenolpyruvate carboxykinase [Escherichia coli] | PF01293 gi 606337 gb AAA58 200.1 | 118.1 99% | 55 55 | 219 360 |
| HNFBK77 | 576186 | 3890 | HMMER 2.1.1 blastx.14 | PFAM: Aldehyde dehydrogenase family serine/threonine kinase with SH3 domain, leucine 1 | PF00171 gi 758593 emb CAA8 8531.1 | 30.2 28% 46% 46% 25% 41% | 231 248 43 371 79 176 | 326 331 81 415 186 211 |
| HNFBQ01 | 938114 | 3897 | | | | | | |
| HNFBW14 | 939763 | 3908 | HMMER 2.1.1 | PFAM: Latrophilin/CL-1- like GPS domain | PF01825 | 35.1 | 44 | 196 |

| | | | blastx.2 | (AF166382) serpentine receptor [Mus musculus] | gb AAF00617.1 AF1 66382.1 | 44% | 38 | 283 |
|---------|--------|------|----------------|--|---|-------------------|------------------|-------------------|
| HNF1G07 | 918389 | 3921 | blastx.14 | (AF128881) PI3 kinase regulatory subunit P101 [Homo sapiens] | gi 4928058 gb AAD3 3397.1 AF128881.1 | 80% 60% | 2 448 | 445 477 |
| HNF1P50 | 965283 | 3936 | blastx.14 | mutant sterol regulatory element binding protein-2 1 | gi 841318 gb AAA85 718.1 | 65% 34% 85% | 356 42 665 | 631 128 685 |
| HNGAL92 | 953889 | 3976 | blastx.14 | phosphatidylserine decarboxylase [Escherichia coli] | gi 551827 gb AAA83 896.1 | 73% | 212 | 18 |
| HNGAS51 | 773208 | 3984 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF000099 | 2.57 | 144 | 182 |
| HNGBF80 | 574475 | 4001 | HMMER 1.8 | PFAM: Zinc finger, C2H2 type | PF000096 | 4.98 | 88 | 111 |
| HNGBH77 | 577361 | 4005 | HMMER 1.8 | PFAM: ATP synthase A chain | PF00119 | 9.81 | 130 | 189 |
| HNGCE85 | 970738 | 4039 | blastx.14 | hypothetical protein Tigger 2 - human transposon MER37.1 | pir S72489 S72489 | 72% 63% | 284 212 | 210 180 |
| HNGCX07 | 953900 | 4065 | HMMER 1.8 | PFAM: Src homology domain 3 | PF00018 | 3.68 | 45 | 161 |
| HNGEN37 | 663955 | 4160 | HMMER 2.1.1 | PFAM: Indole-3-glycerol phosphate synthases | PF00218 | 125.4 | 2 | 223 |
| HNGEQ07 | 953647 | 4169 | HMMER 1.8 | PFAM: TPR Domain | PF00515 | 10.86 | 164 | 238 |
| HNGER43 | 699391 | 4173 | HMMER 1.8 | PFAM: Bacterial mutT protein | PF00293 | 3.79 | 151 | 195 |
| HNGER96 | 922996 | 4177 | blastx.14 | Bkm-like protein [Drosophila melanogaster] | gi 552132 gb AAA28 872.1 | 60% 64% | 250 250 | 294 291 |

| | | | | | | | | | | |
|---------|--------|------|--------------|--|--|------------------------------|--|--------|-----|-----|
| HNGEW76 | 572874 | 4198 | HMMER 1.8 | | PFAM: Helicases conserved C-terminal domain | PF00271 | | 64% | 250 | 291 |
| | | | | | | | | 75% | 215 | 250 |
| | | | | | | | | 80% | 28 | 57 |
| HNGEX35 | 959230 | 4200 | blastx.14 | | adenine phosphoribosyltransferase [Escherichia coli] | gi 1773151 gb AAB4 0223.1 | | 98% | 205 | 366 |
| HNGEX95 | 572897 | 4202 | HMMER 1.8 | | PFAM: Zinc finger, C2H2 type | PF00096 | | 5.32 | 196 | 219 |
| HNGFG22 | 573084 | 4224 | HMMER 1.8 | | PFAM: Bacterial regulatory proteins, luxR family | PF00196 | | 9.2 | 166 | 240 |
| HNGFG69 | 926873 | 4227 | blastx.14 | | collagen [Ascaris suum] | gi 159657 gb AAA29 371.1 | | 44% | 228 | 175 |
| | | | | | | | | 40% | 145 | 80 |
| | | | | | | | | 40% | 145 | 80 |
| | | | | | | | | 40% | 307 | 248 |
| | | | | | | | | 50% | 67 | 38 |
| HNGFK28 | 544726 | 4234 | HMMER 1.8 | | PFAM: ABC transporters | PF00005 | | 86.07 | 445 | 654 |
| | | | blastx.2 | | MsbA protein. [Escherichia coli] | dbj BAA35658.1 | | 100% | 1 | 651 |
| | | | | | | | | 86% | 654 | 989 |
| HNGFK28 | 566798 | 9584 | HMMER 1.8 | | PFAM: ABC transporters | PF00005 | | 86.07 | 445 | 654 |
| | | | blastx.2 | | MsbA protein. [Escherichia coli] | dbj BAA35658.1 | | 100% | 1 | 651 |
| | | | | | | | | 100% | 654 | 989 |
| HNGFK28 | 943114 | 9585 | HMMER 1.8 | | PFAM: ABC transporters | PF00005 | | 117.67 | 342 | 1 |
| | | | blastx.2 | | MsbA protein. | dbj BAA35658.1 | | 100% | 165 | 503 |

| | | | | | | | | |
|---------|--------|------|----------------|--|------------------------------|--|---|---|
| HNGFK28 | 943115 | 9586 | HMMER 2.1.1 | [Escherichia coli] PFAM: ABC transporter transmembrane region. | PF00664 | 84% 91% | 25 2 | 162 37 |
| | | | blastx.2 | | | | | |
| HNGFO46 | 935135 | 4244 | blastx.14 | [Escherichia coli] Msba protein. hypothetical protein T23G5.2 - Caenorhabditis elegans | pir S28303 S28303 | 44% 60% 40% 36% | 84 116 205 263 | 10 87 161 198 |
| | | | HMMER 2.1.1 | | | | | |
| HNGFO81 | 526792 | 4246 | HMMER 2.1.1 | PFAM: Integrase core domain | PF00665 | 42.7 | 84 | 215 |
| HNGFU12 | 971170 | 4265 | HMMER 1.8 | PFAM: RNase H | PF00075 | 55.68 | 102 | 290 |
| | | | blastx.14 | reverse transcriptase (476 AA) [Woolly monkey sarcoma virus] | gi 930259 emb CAA3 3367.1 | 44% 60% | 96 1 | 422 75 |
| HNGFW09 | 924693 | 4270 | blastx.14 | 180 kDa bullous pemphigoid antigen 2/type XVII collagen [Homo sapiens] | gi 1877435 gb AAB5 1499.1 | 50% 53% 66% 36% 75% 60% 85% 85% 60% 54% 50% 26% | 196 167 155 75 152 335 152 152 196 196 289 131 | 155 129 129 1 129 306 132 132 167 164 248 63 |
| | | | | | | 62% 75% | 152 152 | 129 129 |

| | | | | | | | | |
|---------|--------|------|--------------|---|-----------------------------|------|-----|-----|
| HNGGH78 | 924908 | 4306 | blastx.14 | type VII collagen [Cricetulus griseus] | gi 388625 gb AAA36 968.1 | 75% | 152 | 129 |
| | | | | | | 66% | 155 | 129 |
| | | | | | | 66% | 155 | 129 |
| | | | | | | 60% | 193 | 164 |
| | | | | | | 50% | 356 | 397 |
| | | | | | | 34% | 47 | 115 |
| | | | | | | 42% | 285 | 341 |
| | | | | | | 40% | 288 | 347 |
| | | | | | | 50% | 171 | 206 |
| | | | | | | 58% | 171 | 206 |
| | | | | | | 38% | 6 | 59 |
| | | | | | | 41% | 53 | 103 |
| | | | | | | 50% | 171 | 206 |
| HNGGM10 | 964819 | 4317 | HMMER 1.8 | PFAM: Laminin B (Domain IV) | PF00052 | 0.51 | 424 | 441 |
| HNGGR74 | 765698 | 4340 | HMMER 1.8 | PFAM: Zinc finger, C2H2 type | PF00096 | 6.36 | 14 | 58 |
| HNGHT06 | 935706 | 4450 | blastx.14 | unknown protein [Homo sapiens] | gi 196398 gb AAA8 8020.1 | 50% | 254 | 177 |
| HNGIJ01 | 916748 | 4483 | blastx.14 | ORF2 [Rattus norvegicus] | gi 56588 emb CAA37 645.1 | 50% | 168 | 293 |
| | | | | | | 57% | 280 | 342 |
| | | | | | | 57% | 73 | 114 |
| HNGKE07 | 952221 | 4630 | blastx.14 | collagen type VII [Homo sapiens] | gi 495866 gb AAA58 965.1 | 58% | 336 | 286 |
| | | | | | | 55% | 93 | 40 |
| | | | | | | 47% | 155 | 105 |
| | | | | | | 64% | 327 | 286 |
| | | | | | | 57% | 266 | 225 |
| | | | | | | 32% | 87 | 13 |
| | | | | | | 33% | 81 | 1 |
| | | | | | | 62% | 355 | 332 |
| HNGLE52 | 835972 | 4662 | HMMER | PFAM: | PF00049 | 6.75 | 286 | 318 |

| | | | | | | | | | |
|---------|--------|------|-----------|--|---------------------------|--|-------|-----|-----|
| HNGLG06 | 839088 | 4666 | 1.8 | Insulin/IGF/Relaxin family | PF000005 | | 47.92 | 348 | 599 |
| | | | HMMER 1.8 | PFAM: ABC transporters | | | | | |
| | | | blastx.2 | Hypothetical protein HI0658 [Escherichia coli] | dbj BAA35501.1 | | 99% | 270 | 665 |
| HNGLH82 | 954140 | 4668 | blastx.14 | diaminopimelate decarboxylase [Escherichia coli] | gi 455170 gb AAA83861.1 | | 98% | 416 | 249 |
| | | | | | | | 71% | 193 | 47 |
| | | | | | | | 63% | 258 | 136 |
| HNGMM87 | 806036 | 4715 | HMMER 1.8 | PFAM: ATP synthase A chain | PF00119 | | 8.41 | 237 | 362 |
| HNGOO22 | 953888 | 4762 | blastx.14 | (AE000449) putative xylanase [Escherichia coli] | gi 1790156 gb AAC76742.1 | | 94% | 104 | 3 |
| | | | | | | | 91% | 151 | 116 |
| HNHAI11 | 967668 | 4790 | blastx.14 | p15E carboxyterminal sequence [Kirsten murine sarcoma virus] | gi 4469304 emb CAA25493.1 | | 38% | 262 | 161 |
| | | | | | | | 28% | 406 | 323 |
| | | | | | | | 53% | 310 | 272 |
| HNHBE19 | 724404 | 4798 | HMMER 1.8 | PFAM: Helicases conserved C-terminal domain | PF00271 | | 4.4 | 113 | 145 |
| HNHBY45 | 774280 | 4823 | HMMER 1.8 | PFAM: ATP synthase A chain | PF00119 | | 8.4 | 228 | 347 |
| HNHDM74 | 506621 | 4878 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | | 1.89 | 395 | 427 |
| HNHDY50 | 924211 | 4910 | blastx.14 | unknown protein [Homo sapiens] | gi 1196398 gb AAA88020.1 | | 50% | 33 | 170 |
| | | | | | | | 44% | 23 | 169 |
| | | | | | | | 41% | 6 | 164 |
| HNHEJ85 | 964882 | 4955 | blastx.14 | synexin - bovine (fragment) | pir A27695 A27695 | | 54% | 47 | 15 |
| | | | | | | | 46% | 91 | 53 |

| | | | | | | | | |
|---------|--------|------|-----------|---|-------------------------------------|---|---|---|
| HNHET25 | 953410 | 5002 | blastx.14 | (AJ005562) SPR2D protein [Mus musculus] | gi 30933363 emb CAA06591.1 | 40% 38% | 114 91 | 85 53 |
| HNHFA11 | 967126 | 5030 | blastx.14 | (AF144054) apoptosis related protein APR-4 [Homo sapiens] | gi 4868437 gb AAD31316.1 AF144054_1 | 32% 43% 46% | 347 250 207 | 246 203 169 |
| HNHGD07 | 953416 | 5121 | blastx.14 | (AF053091) eyelid [Drosophila melanogaster] | gi 2981221 gb AAC06254.1 | 52% 35% | 212 342 | 355 401 |
| HNHGE09 | 939727 | 5127 | blastx.2 | IDN4-GGTR14 PROTEIN. | sp Q9Y6Y5 Q9Y6Y5 | 46% 55% 33% 30% 50% 36% 26% 62% 42% 62% 83% | 164 227 295 259 346 268 259 367 322 367 367 | 241 280 384 384 381 333 384 390 378 390 384 |
| HNHGH20 | 959499 | 5146 | blastx.14 | notch4 [Homo sapiens] | gi 1841543 gb AAC63097.1 | 81% | 2 | 112 |
| HNHGV22 | 674653 | 5189 | HMMER 1.8 | PFAM: Helicases conserved C-terminal domain | PF00271 | 43% 77% 33% 33% 62% | 56 154 256 297 131 | 9 128 167 244 108 |
| HNHHI10 | 964659 | 5251 | blastx.14 | ORF1 [Rattus norvegicus] | gi 56587 emb CAA37644.1 | 4.66 | 94 | 138 |
| | | | | | | 56% 34% | 75 157 | 28 71 |

| | | | | | | | | | | |
|---------|--------|------|----------------|--|--|---|--|-------|-----|-----|
| HNHHL74 | 765598 | 5266 | HMMER 1.8 | | PFAM: Bacterial mutT protein | PF00293 | | 33% | 220 | 158 |
| HNHIA95 | 908419 | 5318 | HMMER 2.1.1 | | PFAM: gag gene protein p24 (core nucleocapsid protein) | PF00607 | | 63% | 187 | 155 |
| HNHPH29 | 934456 | 5496 | blastx.14 | | (AF118275) atrophin- related protein ARP [Homo sapiens] | gi 4680231 gb AAD2 7584.1 AF118275_1 | | 3.57 | 83 | 148 |
| HOIAE91 | 935322 | 5497 | HMMER 1.8 | | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | | 67.6 | 49 | 300 |
| HSATQ28 | 866951 | 5512 | HMMER 1.8 | | PFAM: Ubiquitin carboxyl-terminal hydrolases family 2 | PF00442 | | 2.66 | 200 | 235 |
| HSAYN79 | 471037 | 5646 | HMMER 1.8 | | PFAM: RNA recognition motif. (aka RRM, RBD, or RNP domain) | PF00076 | | 11.1 | 90 | 122 |
| HSYBL15 | 660053 | 5682 | HMMER 1.8 | | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | | 4.12 | 360 | 380 |
| HSYDP04 | 970789 | 5686 | blastx.14 | | (AF113615) FH1/FH2 domain-containing protein FHOS [Homo sapiens] | gi 5106956 gb AAD3 9906.1 AF113615_1 | | 22.31 | 2 | 70 |
| HT3SA07 | 954360 | 5702 | blastx.14 | | ORF2 contains a reverse transcriptase domain.; ORF2 [Homo sapiens] | gi 339771 gb AAA51 622.1 | | 100% | 77 | 394 |
| HT4GJ85 | 909971 | 5714 | HMMER | | PFAM: PH (pleckstrin) | PF00169 | | 50% | 408 | 467 |
| | | | | | | | | 47% | 393 | 443 |
| | | | | | | | | 50% | 83 | 178 |
| | | | | | | | | 54% | 47 | 79 |
| | | | | | | | | 11.11 | 365 | 451 |

| | | | 1.8 | homology) domain | | | | |
|---------|--------|------|----------------|--|---|------------|------------|------------|
| | | | blastx.14 | (AF053974) SWAP-70 [Mus musculus] | gi 3290154 gb AAC4 0155.1 | 53% | 251 | 448 |
| HTSEA69 | 952359 | 5721 | blastx.14 | (AL032624) cDNA EST yk321h8.5 comes from this gene; 1 from this gene [Caenorhabditis elegans] | gi 3881086 emb CAA 21522.1 | 88% 33% | 4 448 | 54 492 |
| HTAAW46 | 719422 | 5735 | HMMER 1.8 | PFAM: HMG (high mobility group) box | PF00505 | 37% 30% | 264 123 | 479 251 |
| HTABG87 | 940153 | 5745 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF00069 | 5.82 | 6 | 35 |
| | | | blastx.14 | (AF006064) protein kinase homolog [Fowlpox virus] | gi 2393890 gb AAC5 8236.1 | 13.81 | 240 | 335 |
| HTACW17 | 961560 | 5760 | blastx.14 | (AC007660) unknown protein [Arabidopsis thaliana] | gi 4895220 gb AAD3 2806.1 AC007660_7 | 54% 33% | 8 189 | 139 356 |
| HTAFE69 | 944409 | 5797 | blastx.2 | (AK000496) unnamed protein product [Homo sapiens] | dbj BAA91205.1 | 37% 61% | 54 212 | 221 265 |
| HTAHL45 | 908949 | 5817 | HMMER 2.1.1 | PFAM: SCAN domain | PF02023 | 69% | 432 | 704 |
| | | | blastx.14 | (AC004522) Zn-finger- like protein; similar to Z98745 (PID:g2924250) [Homo sapiens] | gi 3006231 gb AAC0 9486.1 | 228.7 | 268 | 555 |
| HTAHV04 | 926747 | 5826 | blastx.14 | (AC005757) R32611_1 [Homo sapiens] | gi 3688089 gb AAC6 2258.1 | 65% 36% | 220 529 | 534 642 |
| HTAJN08 | 958057 | 5841 | HMMER | PFAM: Helicases | PF00271 | 100% | 3 | 446 |
| | | | | | | 5.49 | 20 | 55 |

| | | | | | | | | |
|---------|--------|------|-------------|--|-------------------------------------|---|---|--|
| HTDAE43 | 971582 | 9597 | 1.8 | conserved C-terminal domain | gi 4868437 gb AAD31316.1 AF144054_1 | 53% | 526 | 296 |
| HTGCH58 | 909849 | 5895 | HMMER 2.1.1 | PFAM: RhoGAP domain | PF00620 | 91.4 | 420 | 797 |
| | | | blastx.14 | carboxyl terminus of the predicted protein shows 1 comes from this gene; cDNA EST EMBL:D32994 comes from this gene | gi 3874826 emb CAA86318.1 | 37% 44% 61% | 420 657 771 | 605 758 809 |
| HTGDM65 | 967158 | 5918 | blastx.14 | SH3 domain binding protein [Rattus norvegicus] | gi 1185397 gb AAA87791.1 | 39% 50% 39% 47% 39% 28% 40% | 127 186 278 186 278 337 260 | 59 139 210 136 210 263 195 |
| HTGDT91 | 974962 | 5921 | HMMER 2.1.1 | PFAM: SpoU rRNA Methylase family | PF00588 | 107.6 | 315 | 638 |
| | | | blastx.14 | alternate gene name yibK [Escherichia coli] | gi 466744 gb AAB18583.1 | 100% 100% 76% 81% | 315 531 457 497 | 467 638 495 529 |
| HTGDW96 | 967030 | 5926 | HMMER 2.1.1 | PFAM: Domain of unknown function | PF01784 | 130.2 | 334 | 711 |
| | | | blastx.14 | (AL034490) similar to yeast ngg1-interacting factor 3 | gi 4008560 emb CAA22481.1 | 60% 43% 37% | 1087 460 385 | 1275 660 513 |

| | | | | | | | | | | |
|---------|--------|------|-----------------------------|--|---|--|--|-------|------|------|
| HTGEL46 | 685425 | 5936 | HMMER 1.8 | [Schizosaccharomyces pombe] | | | | 61% | 361 | 414 |
| | | | | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | | | 28% | 970 | 1065 |
| | | | | | | | | 58% | 1312 | 1347 |
| HTGEQ11 | 967047 | 5944 | HMMER 2.1.1 blastx.14 | PFAM: Cytosol aminopeptidase family | PF00883 | | | 7.26 | 398 | 433 |
| | | | | aminopeptidase A [Escherichia coli] | gi 1054725 emb CAA 60164.1 | | | 95% | 27 | 305 |
| | | | | | | | | 83% | 320 | 391 |
| | | | | | | | | 88% | 1 | 27 |
| HTGER72 | 683469 | 5949 | HMMER 1.8 | PFAM: Src homology domain 3 | PF00018 | | | 2.4 | 174 | 203 |
| HTGFZ03 | 923443 | 5968 | HMMER 2.1.1 blastx.14 | PFAM: RNA polymerase beta subunit (AF025424) RNA polymerase I 127 kDa subunit [Rattus norvegicus] | PF00562 | | | 30.7 | 21 | 110 |
| | | | | | gi 2739048 gb AAB9 4600.1 | | | 76% | 3 | 275 |
| HTGGL23 | 974590 | 5973 | blastx.14 | (AE000218) putative adhesion and penetration protein [Escherichia coli] | gi 1787452 gb AAC7 4286.1 | | | 87% | 3 | 443 |
| HTHCB68 | 660309 | 5996 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | | | 3 | 162 | 209 |
| HTJAB35 | 880424 | 9601 | HMMER 1.8 | PFAM: Ank repeat | PF00023 | | | 35.64 | 242 | 325 |
| HTJMT23 | 948518 | 6056 | blastx.14 | (AF182426) arylacetamide deacetylase [Rattus norvegicus] | gi 5923874 gb AAD5 6394.1 AF182426_1 | | | 58% | 2 | 160 |
| HTOAK34 | 966800 | 6081 | HMMER | PFAM: Eukaryotic protein | PF00069 | | | 32.41 | 1020 | 1190 |

| | | | | | | | | |
|---------|--------|------|------------------|---|-------------------------------|-------|-----|------|
| | | | 1.8 blastx.14 | kinase domain (AF084205) serine/threonine protein kinase TAO1 [Rattus norvegicus] | gi 3452473 gb AAC7 1014.1 | 75% | 954 | 1190 |
| HTODG16 | 909952 | 6108 | HMMER 2.1.1 | PFAM: RasGEF domain | PF00617 | 148.5 | 4 | 402 |
| | | | blastx.14 | CDC25 [Saccharomyces kluuyveri] | gi 171187 gb AAA34 479.1 | 34% | 13 | 399 |
| HTOFT34 | 527144 | 6146 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 4.53 | 235 | 264 |
| HTOHL35 | 537364 | 6173 | HMMER 1.8 | PFAM: Zinc finger, C2H2 type | PF00096 | 6.52 | 4 | 33 |
| HTOIY09 | 836003 | 6201 | HMMER 1.8 | PFAM: Insulin/IGF/Relaxin family | PF00049 | 7.08 | 61 | 123 |
| HTSHF47 | 720403 | 6229 | HMMER 1.8 | PFAM: Helix-loop-helix DNA-binding domain | PF00010 | 7.82 | 105 | 140 |
| HTSHM38 | 972248 | 6230 | HMMER 2.1.1 | PFAM: EGF-like domain | PF00008 | 72 | 299 | 406 |
| | | | blastx.14 | (AB011532) MEGF6 [Rattus norvegicus] | gi 3449294 dbj BAA3 2462.1 | 88% | 287 | 538 |
| | | | | | | 50% | 278 | 460 |
| | | | | | | 53% | 320 | 466 |
| | | | | | | 42% | 299 | 460 |
| | | | | | | 42% | 287 | 442 |
| | | | | | | 43% | 290 | 427 |
| | | | | | | 40% | 341 | 481 |
| | | | | | | 46% | 287 | 415 |
| | | | | | | 70% | 114 | 173 |
| | | | | | | 66% | 413 | 457 |

| | | |
|-----|-----|-----|
| 50% | 467 | 532 |
| 61% | 245 | 283 |
| 35% | 188 | 280 |
| 47% | 482 | 538 |
| 52% | 245 | 295 |
| 39% | 476 | 544 |
| 61% | 245 | 283 |
| 31% | 188 | 283 |
| 50% | 245 | 286 |
| 29% | 170 | 280 |
| 55% | 230 | 283 |
| 69% | 245 | 283 |
| 53% | 245 | 283 |
| 50% | 485 | 532 |
| 35% | 452 | 535 |
| 47% | 482 | 532 |
| 47% | 482 | 532 |
| 50% | 245 | 304 |
| 31% | 299 | 412 |
| 70% | 251 | 280 |
| 58% | 251 | 286 |
| 30% | 434 | 532 |
| 58% | 245 | 280 |
| 53% | 245 | 283 |
| 37% | 245 | 316 |
| 63% | 317 | 349 |
| 75% | 245 | 268 |
| 47% | 245 | 295 |
| 37% | 251 | 322 |
| 54% | 251 | 283 |
| 31% | 320 | 406 |

| | | |
|-----|-----|-----|
| 36% | 230 | 286 |
| 40% | 401 | 460 |
| 60% | 203 | 232 |
| 54% | 473 | 505 |
| 34% | 308 | 376 |
| 50% | 245 | 280 |
| 25% | 329 | 445 |
| 62% | 245 | 268 |
| 37% | 485 | 532 |
| 29% | 251 | 343 |
| 50% | 227 | 262 |
| 45% | 251 | 283 |
| 24% | 296 | 406 |
| 71% | 485 | 505 |
| 40% | 473 | 532 |
| 33% | 344 | 406 |
| 71% | 359 | 379 |
| 50% | 245 | 280 |
| 60% | 454 | 483 |
| 62% | 245 | 268 |
| 33% | 491 | 544 |
| 33% | 320 | 382 |
| 63% | 344 | 376 |
| 62% | 359 | 382 |
| 71% | 203 | 223 |
| 45% | 203 | 235 |
| 37% | 215 | 262 |
| 37% | 359 | 406 |
| 38% | 356 | 409 |
| 36% | 320 | 376 |
| 40% | 320 | 379 |

| | | | | | | | | |
|---------|--------|------|----------------|---|-------------------------------|-------|-----|-----|
| HTWCG65 | 869547 | 6260 | HMMER 1.8 | PFAM: Core histones H2A, H2B, H3 and H4 | PF00125 | 60% | 251 | 280 |
| HTWEY30 | 918641 | 6299 | blastx.14 | (AF036548) RGC-32 [Rattus norvegicus] | gi 3800742 gb AAC6 8839.1 | 15.45 | 220 | 306 |
| HTWJA59 | 812705 | 6314 | HMMER 1.8 | PFAM: Helicases conserved C-terminal domain | PF00271 | 88% | 613 | 434 |
| HTXCY84 | 924996 | 6359 | HMMER 2.1.1 | PFAM: Aldehyde dehydrogenase family | PF00171 | 4.95 | 172 | 219 |
| HTXDW14 | 966588 | 6366 | blastx.14 | (AF038838) proline dehydrogenase [Klebsiella aerogenes] | gi 2766693 gb AAB9 5478.1 | 23.9 | 104 | 217 |
| HTXDX61 | 784768 | 6367 | HMMER 2.1.1 | (AB029335) HrPET-3 [Halocynthia roretzi] | gi 5360271 dbj BAA8 1908.1 | 78% | 47 | 241 |
| HTXFN69 | 869397 | 6394 | HMMER 1.8 | PFAM: Amidase | PF01425 | 45% | 16 | 48 |
| HTXGL73 | 529745 | 6403 | HMMER 1.8 | PFAM: HMG (high mobility group) box | PF00505 | 41% | 20 | 70 |
| HTXJL68 | 912611 | 6420 | blastx.14 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 54% | 869 | 777 |
| HTXJM73 | 783572 | 6425 | HMMER 1.8 | RAB14 [Rattus norvegicus] | gi 206535 gb AAA41 994.1 | 45% | 773 | 663 |
| HTXKQ55 | 947789 | 6453 | HMMER 2.1.1 | PFAM: Bacterial mutT protein | PF00293 | 123.2 | 61 | 330 |
| | | | | PFAM: Peptidase family M3 | PF01432 | 6.76 | 72 | 137 |
| | | | | | | 2.21 | 144 | 176 |
| | | | | | | 97% | 230 | 370 |
| | | | | | | 60% | 367 | 450 |
| | | | | | | 59% | 482 | 547 |
| | | | | | | 52% | 373 | 429 |
| | | | | | | 2.87 | 97 | 123 |
| | | | | | | 50.1 | 3 | 299 |

| | | | | | | | | |
|---------|--------|------|-------------|---|-------------------------------------|---------------------------|--------------------------|--------------------------|
| | | | blastx.14 | mitochondrial intermediate peptidase precursor [Homo sapiens] | gi 1763642 gb AAC51231.1 | 96% 100% | 3 335 | 302 367 |
| HTXNY74 | 918076 | 6525 | blastx.14 | (AF078856) p47 [Homo sapiens] | gi 5531827 gb AAD44488.1 | 89% 96% | 93 2 | 530 94 |
| HTXPT68 | 870074 | 6555 | HMMER 2.1.1 | PFAM: NOL1/NOP2/sun family | PF01189 | 43.1 | 29 | 196 |
| HTXQC36 | 961161 | 6560 | blastx.14 | (AB012223) ORF2 [Canis familiaris] | gi 2981631 dbj BAA25253.1 | 51% 57% 60% 42% | 9 326 145 170 | 143 382 174 247 |
| HTXRM86 | 975072 | 6575 | HMMER 2.1.1 | PFAM: Prokaryotic DNA topoisomerase | PF01131 | 99 | 243 | 446 |
| HTXSB88 | 914627 | 6577 | blastx.14 | DNA topoisomerase III (EC 5.99.1.-) [Escherichia coli] | gi 1742870 dbj BAA15551.1 | 51% 40% | 177 3 | 440 158 |
| HTXSR92 | 973095 | 6579 | blastx.2 | (AF077042) 30S ribosomal protein S7 homolog [Homo sapiens] | gi 4689132 gb AAD27775.1 AF077042_1 | 84% | 559 | 771 |
| HUJAM39 | 911399 | 6586 | blastx.14 | (AB016962) synGAP-b1 [Rattus norvegicus] | dbj BAA74972.1 | 60% 55% | 302 1 | 421 60 |
| HUJCM08 | 957784 | 6589 | blastx.14 | (AF051325) SH3 domain containing adaptor protein [Homo sapiens] | gi 4091782 gb AAC99298.1 | 46% 32% | 170 709 | 310 885 |
| HUJAV06 | 966816 | 6597 | blastx.14 | (AF015950) telomerase reverse transcriptase [Homo sapiens] | gi 2330017 gb AAC51672.1 | 100% | 2 | 244 |
| | | | blastx.14 | (AF151854) CGI-96 protein [Homo sapiens] | gi 4929661 gb AAD34091.1 AF151854_1 | 88% 100% 68% 36% | 595 464 537 561 | 521 396 481 487 |

| | | | | | | | | |
|----------|--------|------|-----------------------------|--|--------------------------------------|--------------------|-------------------|-------------------|
| HWAAF66 | 908541 | 6612 | HMMER 2.1.1 blastx.14 | PFAM: KRAB box repressor protein [Homo sapiens] | PF01352 gi 2789430 dbj BAA24380.1 | 65.3 | 90 | 278 |
| HWAAAY03 | 923734 | 6619 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 2.21 | 332 | 373 |
| HWACA38 | 943074 | 6637 | HMMER 1.8 blastx.14 | PFAM: Bacterial mutT protein (AL033536) predicted using Genefinder; similar to 1 1 1 elegans] | PF00293 gi 3947651 emb CAA22138.1 | 3.68 39% 52% | 344 251 766 | 376 433 834 |
| HWADF26 | 957347 | 6656 | HMMER 1.8 blastx.2 | PFAM: Lectin C-type domain short and long forms (AF175206) lectin-like receptor F1 [Homo sapiens] | PF00059 gb AAAF37804.1 AF175206_1 | 104.26 100% | 859 3 | 509 596 |
| HWAEN20 | 868490 | 6691 | HMMER 1.8 | PFAM: Zinc finger, C2H2 type | PF00096 | 6.01 | 251 | 313 |
| HWAFW39 | 947915 | 6697 | HMMER 2.1.1 blastx.2 | PFAM: Peptidase family M1 (AF106037) adipocyte-derived leucine aminopeptidase [Homo sapiens] | PF01433 gb AAAF07395.1 AF106037_1 | 79.5 96% | 200 200 | 367 367 |
| HWAFX39 | 907631 | 6698 | blastx.14 | Zn-binding protein [Pleurodeles waltl] | gi 213868 gb AAA49614.1 | 46% 50% | 118 19 | 354 120 |
| HWAGM33 | 888685 | 6710 | HMMER 2.1.1 | PFAM: Plexin repeat | PF01437 | 25.8 | 898 | 1035 |

| | | | | | | | | |
|---------|--------|------|-----------|--|-------------------------------------|-------|------|------|
| HWAGX37 | 959586 | 6711 | blastx.14 | unknown protein [Homo sapiens] | gi 1196433 gb AAA88038.1 | 47% | 215 | 283 |
| | | | | | | 34% | 535 | 639 |
| | | | | | | 42% | 409 | 471 |
| | | | | | | 29% | 295 | 396 |
| HWAHI10 | 960646 | 6714 | blastx.14 | retinoid X receptor interacting protein [Mus musculus] | gi 709961 gb AAC52167.1 | 62% | 1215 | 583 |
| | | | | | | 66% | 513 | 343 |
| | | | | | | 45% | 642 | 412 |
| | | | | | | 44% | 1272 | 1198 |
| | | | | | | 66% | 1824 | 1798 |
| HWAHS94 | 909667 | 6715 | blastx.14 | (AF151363) Cdc42 GTPase-activating protein [Mus musculus] | gi 5020264 gb AAD38043.1 AF151363_1 | 63% | 278 | 484 |
| | | | | | | 75% | 487 | 510 |
| HWBAL44 | 959449 | 6720 | blastx.14 | (AF151877) CGI-119 protein [Homo sapiens] | gi 4929707 gb AAD34114.1 AF151877_1 | 100% | 531 | 424 |
| HWBAQ16 | 868363 | 6722 | HMMER 1.8 | PFAM: RNA recognition motif. (aka RRM, RBD, or RNP domain) | PF000076 | 4.8 | 857 | 898 |
| HWBBR65 | 747723 | 6741 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF000099 | 4.15 | 185 | 205 |
| HWBDM24 | 963498 | 6771 | blastx.14 | (AJ388555) hypothetical protein [Canis familiaris] | gi 5441611 emb CAB46854.1 | 83% | 908 | 997 |
| | | | | | | 100% | 990 | 1040 |
| | | | | | | 88% | 837 | 863 |
| HWBEX27 | 682583 | 6785 | HMMER 1.8 | PFAM: Helix-loop-helix DNA-binding domain | PF00010 | 38.64 | 184 | 336 |
| HYAAF33 | 915050 | 6820 | blastx.14 | (AF121858) sorting nexin 8 [Homo sapiens] | gi 4689256 gb AAD27831.1 AF121858_1 | 81% | 273 | 434 |
| | | | | | | 96% | 217 | 306 |
| | | | | | | 36% | 172 | 270 |
| HYAAS08 | 926017 | 6831 | blastx.14 | ORF-3 protein [Pseudorabies virus] | gi 334072 gb AAA47471.1 | 62% | 203 | 156 |
| | | | | | | 34% | 84 | 7 |
| | | | | | | 36% | 125 | 69 |
| | | | | | | 63% | 150 | 118 |

| | | | | | | | | |
|---------|--------|------|----------------|---|---|------|-----|-----|
| HYABP53 | 971448 | 6848 | HMMER 2.1.1 | PFAM: Immunoglobulin domain | PF00047 | 37% | 282 | 211 |
| HYABB43 | 800006 | 6860 | HMMER 2.1.1 | PFAM: Alpha-2- macroglobulin family | PF00207 | 27.8 | 257 | 427 |
| | | | blastx.2 | alpha-2-macroglobulin [Mus musculus] | gb AAA39508.1 | 90.9 | 206 | 27 |
| HYAAU65 | 909956 | 6863 | HMMER 2.1.1 | PFAM: RasGEF domain | PF00617 | 67% | 263 | 36 |
| HWBEG18 | 909798 | 6883 | HMMER 2.1.1 | PFAM: EF hand | PF00036 | 47 | 2 | 112 |
| | | | blastx.14 | (AF106071) ras activator RasGRP [Homo sapiens] | gi 4038292 gb AAC9 7349.1 | 33.3 | 505 | 591 |
| HWBCS08 | 909031 | 6897 | HMMER 2.1.1 | PFAM: B-box zinc finger. | PF00643 | 71% | 698 | 889 |
| | | | blastx.14 | (AF119043) transcriptional intermediary factor 1 gamma; TIF1 gamma [Homo sapiens] | gi 4325109 gb AAD1 7259.1 | 59% | 382 | 597 |
| HWBAQ71 | 944080 | 6918 | blastx.2 | predicted using GeneFinder [Caenorhabditis elegans] | emb CAA97423.1 | 46% | 103 | 420 |
| HWAFG12 | 969605 | 6934 | blastx.14 | (AF071081) proline-rich mucin homolog [Mycobacterium tuberculosis] | gi 5305335 gb AAD4 1594.1 AF071081_1 | 70% | 604 | 684 |
| | | | | | | 48% | 2 | 142 |
| | | | | | | 66% | 619 | 654 |
| | | | | | | 32.5 | 263 | 388 |
| | | | | | | 92% | 2 | 562 |
| | | | | | | 34% | 141 | 464 |
| | | | | | | 34% | 112 | 17 |
| | | | | | | 50% | 195 | 142 |
| | | | | | | 28% | 398 | 264 |
| | | | | | | 40% | 365 | 300 |

| | | | | | | | | |
|---------|--------|------|--------------------------|---|---------------------------|--------|-----|-----|
| HWAFA47 | 948858 | 6938 | blastx.2 | (AF010144) neuronal thread protein AD7c-NTP [Homo sapiens] | gb AAC08737.1 | 34% | 219 | 142 |
| | | | | | | 44% | 154 | 101 |
| | | | | | | 32% | 374 | 300 |
| | | | | | | 34% | 365 | 297 |
| | | | | | | 34% | 332 | 264 |
| | | | | | | 63% | 338 | 306 |
| | | | | | | 29% | 365 | 294 |
| | | | | | | 38% | 314 | 261 |
| | | | | | | 59% | 208 | 14 |
| | | | | | | 50% | 178 | 14 |
| HWAEU35 | 887166 | 6942 | HMMER 2.1.1 blastx | PFAM: Immunoglobulin domain CMRF-35 antigen [Homo sapiens] | PF00047 emb CAA46948.1 | 40% | 253 | 80 |
| | | | | | | 77% | 78 | 13 |
| | | | | | | 52% | 93 | 25 |
| | | | | | | 76% | 249 | 211 |
| | | | | | | 42% | 221 | 165 |
| | | | | | | 75% | 240 | 205 |
| | | | | | | 42% | 237 | 160 |
| | | | | | | 90% | 357 | 328 |
| | | | | | | 25% | 248 | 168 |
| | | | | | | 23.2 | 40 | 273 |
| HWAEG71 | 931547 | 6946 | HMMER 1.8 blastx.2 | PFAM: Ras family (contains ATP/GTP binding P-loop) rab-related GTP-binding protein [Rattus] | PF00071 gb AAA42000.1 | 55% | 7 | 162 |
| | | | | | | 59% | 169 | 279 |
| | | | | | | 60% | 400 | 474 |
| | | | | | | 38% | 346 | 399 |
| | | | | | | 42% | 316 | 372 |
| | | | | | | 147.95 | 116 | 475 |
| | | | | | | 98% | 86 | 493 |
| | | | | | | 80% | 477 | 569 |

| HWAEC08 | 958115 | 6947 | HMMER 2.1.1 | norvegicus] PFAM: Spectrin repeat | PF00435 | 29.5 | 3 | 215 |
|---------|--------|------|----------------|--|---|-------|-----|-----|
| | | | | | | | | |
| | | | blastx.14 | (AL080133) hypothetical protein [Homo sapiens] | gi 5262574 emb CAB 45729.1 | 69% | 12 | 209 |
| | | | | | | 70% | 381 | 452 |
| | | | | | | 31% | 18 | 209 |
| | | | | | | 29% | 228 | 308 |
| HWACY70 | 756888 | 6956 | HMMER 2.1.1 | PFAM: RIO1/ZK632.3/MJ0444 family | PF01163 | 96 | 280 | 552 |
| HWABG11 | 949088 | 6971 | HMMER 2.1.1 | PFAM: Glucosamine-6- phosphate isomerase | PF01182 | 225.7 | 67 | 381 |
| | | | blastx.2 | unnamed protein product [unidentified] | emb CAA03416.1 | 91% | 67 | 480 |
| HUUDR34 | 944903 | 6984 | blastx.14 | similar to SH3-binding protein [Homo sapiens] | gi 4826478 emb CAB 42896.1 | 82% | 2 | 550 |
| | | | | | | 100% | 571 | 594 |
| | | | | | | 77% | 552 | 578 |
| | | | | | | 100% | 596 | 616 |
| HUUCJ02 | 940813 | 6986 | blastx.14 | (AF132984) nuclear pore complex interacting protein NP1P [Homo sapiens] | gi 4959568 gb AAD3 4394.1 AF132984_1 | 99% | 770 | 417 |
| | | | | | | 89% | 417 | 250 |
| | | | | | | 71% | 300 | 187 |
| | | | | | | 58% | 226 | 119 |
| | | | | | | 87% | 278 | 231 |
| | | | | | | 100% | 261 | 226 |
| | | | | | | 54% | 261 | 196 |
| | | | | | | 60% | 258 | 199 |
| | | | | | | 81% | 181 | 149 |
| | | | | | | 83% | 152 | 117 |
| | | | | | | 40% | 229 | 149 |
| | | | | | | 100% | 152 | 126 |
| | | | | | | 90% | 192 | 163 |

| | | | | | | | | |
|---------|--------|------|----------------|---|-------------------------------|--|--|--|
| HTXOO15 | 869261 | 7011 | HMMER 2.1.1 | PFAM: Ubiquitin family | PF00240 | 66% | 300 | 274 |
| HTXLS08 | 958357 | 7023 | blastx.14 | (AF090989) high-risk human papilloma viruses E6 1 alpha [Homo sapiens] | gi 4151328 gb AAD1 2543.1 | 48% 68% 41% 57% 70% 27% | 745 1006 1 511 427 580 | 987 1146 237 645 477 645 |
| HTWKB07 | 952841 | 7085 | blastx.14 | (AF003535) ORF2-like protein [Homo sapiens] | gi 2197085 gb AAD0 4635.1 | 60% 75% 50% 33% 70% | 25 259 205 36 167 | 84 294 258 116 196 |
| HTWJH08 | 790185 | 7087 | blastx.2 | (AK000385) unnamed protein product [Homo sapiens] | dbj BAA91131.1 | 61% | 197 | 51 |
| HTWJH08 | 846554 | 9615 | blastx.2 | (AK000385) unnamed protein product [Homo sapiens] | dbj BAA91131.1 | 61% | 197 | 51 |
| HTWJF50 | 911448 | 7089 | blastx.14 | myosin I [Rattus norvegicus] | gi 3724141 emb CAA 50871.1 | 48% 53% 55% 46% 39% 50% | 1009 334 732 863 40 686 | 1428 681 851 1012 108 715 |
| HTWFQ19 | 586124 | 7091 | HMMER 2.1.1 | PFAM: Sema domain | PF01403 | 62.9 | 14 | 184 |
| HTOIA82 | 844319 | 7198 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 4.25 | 50 | 82 |
| HTOHI14 | 659280 | 7204 | HMMER | PFAM: Asparaginase | PF01112 | 20.7 | 140 | 217 |

| | | | | | | | | |
|---------|--------|------|--------------------|---|--|--------------------------|------------------------|-------------------------|
| HTODM08 | 960113 | 7222 | 2.1.1 blastx.14 | (AF106069) deubiquitinating enzyme [Homo sapiens] | gi 5814097 gb AAD5 2099.1 AF106069_1 | 33% | 5 | 367 |
| HTHBY73 | 946168 | 7282 | blastx.2 | (AK001868) unnamed protein product [Homo sapiens] | dbj BAA91951.1 | 52% 45% | 4 162 | 183 332 |
| HTGEX10 | 963862 | 7305 | HMMER 2.1.1 | PFAM: SET domain | PF00856 | 105.2 | 580 | 960 |
| HTGEA37 | 908606 | 7311 | blastx.14 | (AC005065) determined by GENSCAN prediction and 1 | gi 4153862 gb AAD0 4721.1 | 65% 40% | 601 337 | 1017 477 |
| HTAIF22 | 910040 | 7364 | HMMER 2.1.1 | (AF001293) aiolos [Mus musculus] PFAM: RhoGEF domain | gi 2150044 gb AAB5 8795.1 PF00621 | 80% | 1 | 216 |
| HTAIF11 | 965738 | 7365 | blastx.14 | (AL022271) similar to Guanine nucleotide exchange 1 1 1 this g | gi 3876654 emb CAA 18349.1 | 64% | 281 | 397 |
| HTAEV23 | 959129 | 7369 | HMMER 2.1.1 | (AF061555) ubiquitin- protein ligase E3-alpha [Mus musculus] PFAM: WW domain | gi 3170887 gb AAC4 0165.1 PF00397 | 48% 50% | 6 297 | 293 392 |
| HTAEP05 | 932459 | 7370 | blastx.14 | This gene is novel. [Homo sapiens] Pro-Pol-dUTPase polyprotein [Mus musculus] | gi 603953 dbj BAA07 893.1 gi 2065210 emb CAA 73251.1 | 89% | 823 | 359 |
| | | | | | | 76% 48% 47% 44% | 225 406 3 500 | 275 510 59 553 |

| | | | | | | | | |
|---------|--------|------|----------------|--|-------------------------------|-------|-----|-----|
| HTABK47 | 720684 | 7379 | HMMER 2.1.1 | PFAM: Monooxygenase | PF01360 | 77% | 386 | 412 |
| HSYCV01 | 940661 | 7408 | HMMER 1.8 | PFAM: Hydroxymethylglutaryl- coenzyme A reductase | PF00369 | 7.29 | 448 | 492 |
| HSAWR08 | 959943 | 7458 | blastx.14 | (AL110271) hypothetical protein [Homo sapiens] | gi 5817084 emb CAB 53709.1 | 98% | 123 | 287 |
| HSAUL84 | 908440 | 7504 | HMMER 2.1.1 | PFAM: gag gene protein p24 (core nucleocapsid protein) | PF00607 | 43.3 | 105 | 302 |
| HNHOF94 | 948720 | 7551 | blastx.14 | gag protein [Human endogenous retrovirus K.] | gi 1780975 emb CAA 71418.1 | 83% | 135 | 299 |
| | | | blastx.2 | (AK000496) unnamed protein product [Homo sapiens] | dbj BAA91205.1 | 60% | 24 | 152 |
| HNHNP81 | 928378 | 7554 | HMMER 1.8 | PFAM: 7 transmembrane receptor (rhodopsin family) | PF00001 | 58.09 | 233 | 511 |
| | | | blastx.2 | (AF091575) olfactory receptor [Rattus norvegicus] | gb AAC64595.1 | 61% | 236 | 505 |
| HNHLC01 | 915363 | 7581 | blastx.14 | unknown protein [Homo sapiens] | gi 1196431 gb AAA8 8036.1 | 52% | 502 | 618 |
| | | | blastx.2 | (AK000385) unnamed protein product [Homo sapiens] | dbj BAA91131.1 | 46% | 5 | 82 |
| HNHGV62 | 743400 | 7603 | blastx.2 | | | 40% | 57 | 131 |
| | | | | | | 36% | 133 | 207 |
| | | | | | | 61% | 219 | 257 |
| | | | | | | 46% | 260 | 304 |
| | | | | | | 62% | 52 | 285 |
| | | | | | | 76% | 287 | 349 |

| | | | | | | | | |
|---------|--------|------|----------------|--|------------------------------|----------------------|-------------------|-------------------|
| HNHGE31 | 698046 | 7624 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 3.3 | 83 | 109 |
| HNHFV49 | 975415 | 7644 | blastx.2 | hypothetical protein (L1H 3' region) - human | pir B34087 B34087 | 81% 71% 90% | 483 227 217 | 190 6 188 |
| HNHFH24 | 903741 | 7657 | HMMER 2.1.1 | PFAM: Sodium:neurotransmitter symporter family | PF00209 | 37.2 | 208 | 306 |
| | | | blastx.14 | (AF075266) orphan transporter isoform B9 [Mus musculus] | gi 3347930 gb AAC2 7761.1 | 76% 27% | 187 414 | 327 467 |
| HNHDF07 | 953883 | 7702 | HMMER 1.8 | PFAM: Fibronectin type III domain | PF00041 | 7.48 | 242 | 319 |
| HNHDC29 | 904546 | 7704 | blastx.14 | contactin associated protein [Homo sapiens] | gi 1857708 gb AAB4 8481.1 | 98% | 219 | 7 |
| HNHCI32 | 861673 | 7716 | HMMER 1.8 | PFAM: 7 transmembrane receptor (rhodopsin family) | PF00001 | 133.17 | 195 | 545 |
| | | | blastx.2 | (AF112461) G protein- coupled receptor 57 [Homo sapiens] | gb AAF27279.1 AF1 12461_1 | 100% 100% 100% | 189 112 56 | 551 186 112 |
| HNHCI32 | 956105 | 9645 | HMMER 1.8 | PFAM: 7 transmembrane receptor (rhodopsin family) | PF00001 | 133.17 | 951 | 601 |
| | | | blastx.2 | (AF112461) G protein- coupled receptor 57 [Homo sapiens] | gb AAF27279.1 AF1 12461_1 | 100% 100% 100% | 555 478 422 | 917 552 478 |
| HNHBF47 | 949027 | 7731 | HMMER 1.8 | PFAM: Cadherin | PF00028 | 44.76 | 668 | 522 |
| | | | blastx.2 | (AB028499) Flamingo 1 | dbj BAA84070.1 | 96% | 409 | 666 |

[illegible]

| | | | | | | | | | |
|---------|--------|------|--------------|--|---|--|-------|-----|------|
| HNHAF61 | 742116 | 7745 | HMMER 1.8 | PFAM: Cadherin | PF00028 | | 39% | 412 | 480 |
| | | | blastx.2 | (AF152473) protocadherin alpha C1 short form protein [Homo sapiens] | gb AAD43734.1 AF1 52473_1 | | 46.67 | 330 | 461 |
| HNHAF61 | 955094 | 9649 | blastx.14 | (AF152303) protocadherin alpha C1 [Homo sapiens] | gi 5456892 gb AAD4 3697.1 | | 75% | 81 | 677 |
| | | | | | | | 84% | 173 | 364 |
| HNGOZ40 | 969158 | 7757 | blastx.14 | (AF155098) NY-REN-8 antigen [Homo sapiens] | gi 5360091 gb AAD4 2864.1 AF155098_1 | | 33% | 87 | 686 |
| | | | | | | | 93% | 1 | 84 |
| HNGNY02 | 918626 | 7769 | HMMER 1.8 | PFAM: FAD/NAD- binding domain in oxidoreductases | PF00175 | | 40% | 10 | 75 |
| | | | | | | | 98% | 325 | 1071 |
| HNGND01 | 915294 | 7778 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | | 40% | 715 | 987 |
| | | | | | | | 42% | 499 | 660 |
| HNGMW65 | 950173 | 7781 | blastx.2 | (AF010144) neuronal thread protein AD7c-NTP | gb AAC08737.1 | | 32% | 778 | 1023 |
| | | | | | | | 37% | 724 | 867 |
| | | | | | | | 100% | 225 | 275 |
| | | | | | | | 77% | 176 | 229 |
| | | | | | | | 30% | 496 | 684 |
| | | | | | | | 89% | 269 | 325 |
| | | | | | | | 35% | 895 | 1011 |
| | | | | | | | 40% | 568 | 663 |
| | | | | | | | 36% | 717 | 791 |
| | | | | | | | 50% | 499 | 540 |
| | | | | | | | 78% | 599 | 477 |
| | | | | | | | 4.43 | 366 | 440 |
| | | | | | | | 2.07 | 464 | 490 |
| | | | | | | | 62% | 340 | 143 |
| | | | | | | | 67% | 340 | 248 |

| | | | | | | | | |
|---------|--------|------|--------------------------|---|-------------------------------|--|---|--|
| HNGMD48 | 974358 | 7788 | HMMER 1.8 | PFAM: Cystatin domain | PF00031 | 45% 60% 55% 68% 43% 43% 55% 64% 57% 47% | 417 345 80 81 200 414 205 392 202 86 | 247 247 3 25 111 346 152 351 125 18 |
| HNGLY08 | 948825 | 7791 | blastx.14 | (AJ010949) calcium channel alpha-2-delta-C subunit [Mus musculus] | gi 4186073 emb CAA 09423.1 | 79% | 219 | 392 |
| HNGLL07 | 952236 | 7795 | blastx.14 | KERATIN TYPE II CYTOSKELETAL 8 (FRAGMENT). | sp Q29386 Q29386 | 41% 71% 83% 72% | 199 43 77 242 | 77 2 42 210 |
| HNGKM74 | 942758 | 7801 | HMMER 1.8 blastx.2 | PFAM: HMG (high mobility group) box (AL117470) hypothetical protein [Homo sapiens] | PF00505 emb CAB55945.1 | 5.95 40% | 437 2 | 526 817 |
| HNGIR10 | 964715 | 7837 | blastx.14 | NK10 [Mus musculus] | gi 506502 emb CAA5 6225.1 | 61% 62% 54% 52% 54% 53% 50% 44% | 196 193 199 196 193 199 193 196 | 2 2 2 2 2 2 2 8 |

| | | | | | | | | |
|---------|--------|------|-----------|---|----------------------------|-------|-----|-----|
| HNGFF50 | 941480 | 7879 | blastx.14 | (AJ010949) calcium channel alpha-2-delta-C subunit [Mus musculus] | gi 4186073 emb CAA.09423.1 | 45% | 193 | 2 |
| | | | | | | 61% | 199 | 92 |
| | | | | | | 57% | 196 | 83 |
| | | | | | | 37% | 178 | 11 |
| | | | | | | 26% | 217 | 2 |
| | | | | | | 39% | 115 | 2 |
| | | | | | | 46% | 181 | 104 |
| | | | | | | 50% | 232 | 197 |
| | | | | | | 33% | 309 | 256 |
| | | | | | | 30% | 306 | 238 |
| HNGE079 | 951489 | 7897 | HMMER 1.8 | PFAM: IG (immunoglobulin) superfamily | PF00047 | 33.71 | 290 | 466 |
| | | | blastx | (AF143185) high affinity immunoglobulin gamma Fc 1 | gb AAD34946.1 AF143185_1 | 54% | 287 | 385 |
| | | | | | | 41% | 404 | 520 |
| | | | | | | 77% | 230 | 283 |
| | | | | | | 36% | 140 | 214 |
| HNGEI11 | 967314 | 7902 | blastx.14 | pol polyprotein [Baboon endogenous virus] | gi 509838 gb AAA87332.1 | 70% | 258 | 317 |
| | | | | | | 42% | 39 | 152 |
| | | | | | | 53% | 324 | 368 |
| HNGDM11 | 967512 | 7933 | blastx.14 | reverse transcriptase [Homo sapiens] | gi 439877 gb AAB02291.1 | 36% | 381 | 292 |
| | | | | | | 50% | 276 | 205 |
| | | | | | | 47% | 154 | 104 |
| | | | | | | 20% | 210 | 82 |
| HNGDA08 | 959964 | 7952 | HMMER 1.8 | PFAM: Zinc finger, CCHC class | PF00098 | 5.01 | 261 | 284 |
| HNGAZ08 | 959977 | 7973 | blastx.14 | p40 [Homo sapiens] | gi 2072966 gb AAC51272.1 | 45% | 391 | 320 |
| | | | | | | 40% | 93 | 19 |

| | | | | | | | | | |
|---------|--------|------|----------------|---|--|-------------------------------------|---|---|---|
| HNFID11 | 966347 | 7997 | blastx.14 | (AF132948) CGI-14 protein [Homo sapiens] | | gi 4680667 gb AAD27723.1 AF132948_1 | 40% | 144 | 100 |
| HNFHR56 | 733297 | 8003 | HMMER 1.8 | PFAM: IG (immunoglobulin) superfamily | | PF00047 | 100% | 14 | 115 |
| HNEDO77 | 955894 | 8051 | blastx.14 | (AB020063) Keap1 [Mus musculus] | | gi 3894323 dbj BAA34639.1 | 90% 44% 42% 38% 44% 100% 27% 85% | 384 387 420 339 387 79 402 360 | 64 91 91 91 232 44 316 346 |
| HNEBJ81 | 529571 | 8067 | HMMER 2.1.1 | PFAM: N-acetyltransferase | | PF00797 | 40.5 | 18 | 125 |
| HMWEN61 | 909931 | 8125 | blastx.14 | (AF020313) proline-rich protein 48 [Mus musculus] | | gi 2624972 gb AAB94880.1 | 84% 100% | 89 89 | 307 9 |
| HMWBT59 | 893995 | 8141 | HMMER 1.8 | PFAM: 4 transmembrane segments integral membrane proteins | | PF00335 | 27.49 | 51 | 113 |
| HMSMN71 | 927097 | 8184 | HMMER 1.8 | PFAM: Ubiquitin family | | PF00240 | 32.11 | 24 | 200 |
| | | | blastx.14 | (AF176069) ubiquitin [Homo sapiens] | | gi 5733824 gb AAD49751.1 AF176069_1 | 78% 63% 53% | 3 550 550 | 518 606 594 |
| HMSJL53 | 921263 | 8196 | blastx.14 | decorin (PGII) [Mus musculus] | | gi 53669 emb CAA37876.1 | 36% 46% 35% | 281 48 134 | 403 131 244 |